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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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/cgm2_6/ptcdata/1/iaa/f_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/H_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/PCTM2_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/RB_COMB.pep:*
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/08974899;
Patent No. 6037454
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES:
ADDERSENER Genentech, Inc.
STREET: 1 DNA May
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 649; DB 2;
100.0%; Pred. No. 7.7e-57;
cive 0; Mismatches 0;
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ZIP: 94080
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/08/974,899
US-09-355-014-55
US-09-355-014-55
US-09-027-985-70
US-09-027-340A-70
US-09-121-952A-70
US-09-355-014-70
US-09-027-449-60
US-09-027-449-60
US-09-121-952A-60
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US-09-121-952A-60
US-09-121-952A-71
US-09-027-449-71
US-09-027-449-71
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTONNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/225-1994
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Best Local S:
Matches 121;
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GENERAL INFORMATION:
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                                          61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24. Application US/09795798

Patent No. 6703018

GENERAL INFORMATION:

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: WinPatin (Genentech)
COMPUTER: CALON (WINBER: 08/974,899
FILING DATE: CALON (WINBER: PROCK)
CHASSIFICATION NUMBER: Win (WINBER: PROCK)
CHASSIFICATION NUMBER: PROCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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; Pred. No. 7.7e-57;
0; Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 24:
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Patent No. 6037454
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Best Local Similarity 100.0%;
Matches 121; Conservative 0
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                                                                                                                                                                                                                      121 $ 121
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US-08-974-899-5
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61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
CONTEX: USA
ZIP: 94080
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Patent No. 6703018
GENERAL INFORMATION:
TAPLICANT: Presta, Leonard G.
APLICANT: Presta, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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Pred. No. 3.7e-55;
1; Mismatches 3
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIPTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NDATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT IRRORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECHOME: 650/225-1984
TELECHOME: 650/225-1981
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: L-4
974-R0^
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COMPUTER READABLE FORM:
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Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 S 121
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US-09-795-798-5
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STREE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TYPE: Amino Acid

TOPOLOGY: Linear

US-08-804-444A-50
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                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear
US-09-027-449-50
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US-08-804-444A-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BVQLVBSGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.4%; Score 632; DB 2; Length 121; Best Local Similarity 96.7%; Pred. No. 3.7e-55; Matches 117; Conservative 1; Mismatches 3; Indels
                                              SOFTWARE: WIDFALLE CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/9/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: cUnknown>
ATTORNEY/AGENT INPORMATION:
NAMME: Lee, Wendy W.
REGISTRATION NUMBER: 40,378
REPERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
FEMILE COMMATION: 100: 5:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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Sequence 50, Application US/09027449
Patent No. 6025158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 121 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSES: General Col., INC. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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Patent No. 6117980
GENERAL INPORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
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                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
84.5%; Score 548.5; DB 2; Length 1
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels
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88.8%; Pred. No. 6.2e-47;
iive 2; Mismatches 10;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPALIDIE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,444A FILING DATE: 21-Feb-1997 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION: NAME: Love, Richard B. REGISTRATION NUMBER: 91085
REGISTRATION NUMBER: 91085
TELECOMMUNICATION INFORMATION: FILESCOMMUNICATION INFORMATION: TELESCOMMUNICATION INFORMATION:
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34-659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELEPHONE: 650/522-530
TELEPHONE: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
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RESULT 9
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1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                              1 EVQLVESGGGLVQPGGSLRLSCAASGPSPTGHWANWVRQAPGKGLEWVGMIHPSDSETRY 60
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                                                                                                                                  61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                 61 NOKFKDRPTISVDKSKNTLYLOMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gonzalez, Tania R.
APPLICANT: Beong, Steven R.
APPLICANT: Prests. Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
CORRESPONDENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.5%; Score 548.5; DB 2; Length 116;
88.8%; Pred. No. 6.2e-47;
Live 2; Mismatches 10; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei, Vanessa
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard
APPLICANT: Presta, Leonard
APPLICANT: Shahrokh, Zahra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winparin (Genentech)
CURRENT APPLICATION DATA:
PTLING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/225-9881
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                            Sequence 50, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 116 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.89
Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
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| MPRILCANT: Against Generated A. Targets of PREMING INFLAMMATORY DISEASES ITTLE OF INVERTION: METHORS OF TREATING INFLAMMATORY DISEASES ITTLE OF INVERTION: METHORS OF TREATING INFLAMMATORY DISEASES ITTLE OF INVERTION: ADDRESS: 72
| NUMBERS OF SEQUENCES: 73
| APPLICATION OF THE PRINCIPLE PORT: ADDRESS: 73
| COUNTRY: USA | COUNTRY: USA
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1; Gaps

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1 EVOLVESGGGLVQPGGSLRLSCAASGFSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

84.5%; Score 548.5; DB 2; Length 116;
Best Local Similarity 88.8%; Pred. No. 6.2e-47;
Matches 103; Conservative 2; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 13M FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFCATION NUMBER: BCT/US92/05126
FILING DATE: 15-UNM-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 14-UNM-1991
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UNM-1991
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 90,378
REFERENCE/DOCKET NUMBER: 90,0992
TELEOPHONE: 650,025-1994
                                                                             NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
RELECOMMUNICATION INFORMATION:
TELEFAX: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Declared G. Presta
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear; SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-09-355-014-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-934-373C-20
; Sequence 20, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
                                     CLASSIFICATION: <Unkno ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 122 amino acide
TYPE: Amino Acid
TOPOLOGY: Linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ADSVKGRFTISRDNSKNTLYLQMNSLRABDTAVYYCAARGIYFYGTTYFDYWGQGT 116
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Sequence 50, Application US/09355014
Sequence 67003
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
Leong, Steven R.
Presta, Leonard G.
Shahrokh, Zahra
Shahrokh, Zahra
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 116;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 84.5%; Score 548.5; DB 2; Best Local Similarity 88.8%; Pred. No. 6.2e-47; Matches 103; Conservative 2; Mismatches 10;
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07430
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07467
FILING DATE: 20-JAN-1998
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FBB-1998
APPLICATION NUMBER: 34,659
FILING DATE: 20-FBB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REJERRATION NUMBER: 34,659
REJERRATION NUMBER: 34,659
TELEPHONE: 650/225-5530
TELEPHONE: 650/225-5530
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
TENERGALE AND AND ACTOR AND A
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APPLICATION NUMBER: US/09/355,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 116 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
                                                                                                                                 61 NOKEKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGQGTLVT 119
                         1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTWNWVRQAPGKGLEWVALINPYKGVSTY
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TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 122 amino acids
Amino Acid
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Best Local Similarity 83.73
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-146-206C-20
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                                                                                                                                                                                                                           61 NQKFKDRFTISVDKSKNTAYLQMNSLRAEDTAVYYCARSGY-YGDSDWYFDVWGGGTLVT 119
                                                                                                                                                                                                    61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YPDYWGQGTLVT 118
                                                                                                                                                              9
                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTWNWRQAPGKGLEWVALINPYKGVSTY
                                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                   Gaps
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                                       Score 520.5; DB 1; Length 122;
Pred. No. 3.9e-44;
4; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 122;
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Pred. No. 3.9e-44;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/034373
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/15272
FILING DATE: 14-JUN-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P0709P2C1
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REFERENCE/DOCKET NUMBER: PO.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                       Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Best Local Similarity 83.7%;
Matches 103; Conservative
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Amino Acid
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US-07-934-373C-20
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US-08-437-642B-20
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Pred. No. 3.9e-44;
4; Mismatches 13; Indels 3
Sequence 10, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wilpeatin (Genentech) CURRENT APPLICATION DATA: WS/08/146,206C FILING DATE: 17-No. 6407213-1993 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 0/715272 FILING DATE: 14-UTN-1991 ATTORNEY/AGENT INFORMATION:
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61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
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                                                                                                                                Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSE: Genemetech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Patent No. 6719971
GENERAL INPORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES:
ADDRESSER: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.2%; Score 520.5; DB 2; Length 122; 83.7%; Pred. No. 3.9e-44; tive 4; Mismatches 13; Indels 3
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CURRITACATION NOWBER: US/09/705,686
FILING DATE: 0.2-NO. 6639055-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOW-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UNM-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709F1D3
TELECOMMUNICATION INFORMATION:
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                                              Sequence 20, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650/225-1994
TELEPRAK: 650/652-9881
INFORMATION POR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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Best Local Similarity 83.7
Matches 103; Conservative
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RESULT 14
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61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGOGTLVT 118
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nes 13; Indels
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NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFORM SEQ ID NO: 20:

SEQUENCE CHARACTERS STATES:

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TRESTER SEQ ID NO: 20:

SEQUENCE CHARACTER STATES:

TYPE: Amino Acid
                                                                                                                         COMPUTER: 15.5 inch, 1.44 Mb floppy disk COMPUTER: 15.5 inch, 1.44 Mb floppy disk COMPUTER: 15.5 inch, 1.44 Mb floppy disk COMPUTER: 1EM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705, 392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION SATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UNN-1991
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Pred. No. 3.9e
4; Mismatches
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US-09-705-392A-20
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                   CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.2%;
Best Local Similarity 83.7%;
Matches 103; Conservative 9
                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
STREET: 1 DNA Way
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                              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Aeb27726
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Adw33104
Adw3311
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Adw21320
Adx00805
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Adx29454
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ADW03411 AEB27728 ABB27728 ADP79584 ADW03399 ADW03406 ADW21319 ADW21312 ADW21320 ADX29454 AAX29454 AAX77757

Humanized Humanized

Humanized Variable Anti-CD20 Humanized

ALIGNMENTS

Complementarity determining region; heavy chain variable region; humanised antibody; MRM24F(ab)-8; anti-CD11a antibody; human CD11a I domain; MFM24 epitope; alpha subunit; lymphocyte function-associated antigen 1; LFA-1; immunoassay; Rhesusised heavy chain of humanised anti-CD11a antibody in vivo imaging; diagnosis; CD11a-associated disease peptide; 121 AA (first entry) 01-OCT-1998 AAW62019;

04-JUN-1998.

97WO-US019041. 20-OCT-1997;

96US-00757205. 27-NOV-1996;

New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease.

humanised anti-CD1a antibody that binds specifically to the human CD1a I domain (WHM24 epitope). CD1a refers to the alpha subunit of lymphocyte function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-CD11a antibodies are used to determine presence of CD11a in usual immunoassays or by in vivo imaging, particularly for diagnosis of CD11a associated diseases (typically immune responses and inflammation such as poriasis, Crohn's disease, rheumatoid arthritis, transplant rejection, leukaemia, etc

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Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

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Minimum DB Maximum DB

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

2443163 seqs, 439378781 residues

Perfect score:

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Scoring table:

Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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WO9823761-A1.

(GETH) GENENTECH INC.

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AAB30312

ABU13789 ABU59502

Jardieu PM, Presta LG;

WPI; 1998-322737/28.

Humanised Humanised CD11a hea Humanized

anti-CD11

Ady 92348 1
Ady 92012 1
Ady 92380 1
Ady 9232 1
Ady 92389 3
Ady 9238 1
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Ady 92312 1
Ady 9277 7

Human IgG Human IgG Human IgG Human IgG Human IgG Human IgG

Mouse ant

ADS33302 ADW03408 ADW21310

ADP79574

The present sequence represents the heavy chain of a "rhesusised" (sic) Disclosure; Page 56; 66pp; English

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22-JUN-2000
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Conversion to the mutant form allows useful antibodies to be produced
                                                                                                                            120
                                                                                                                                       61 NQKPKDRPTISVDKSKONTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutants of species-dependent antibodies with affinity for non-human mammalian antigen - greater than for parent antibody, particularly used for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                          61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                         1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNNWVRQAPGKGLEWVGMIAPASSSTRY
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                        Score 649; DB 2;
Pred. No. 1.7e-49;
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                                                0; Mismatches
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                                                                                                                                                                                                                                                                AAW63542 standard; protein; 121 AA.
                        100.0%;
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                                                                                                                                                                                                                                                                                                                 (first entry)
                                             Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directed against CD11a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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                       Query Match
Best Local Similarity
 Sequence 121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                          AAW63542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitiramily inflammation; immunological response; LFA-1; lymphocyte function-associated antigen-1; psortlasis; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
                                                                                                                                                                                                                                                                                                                                           EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                             EVOLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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from antibodies which normally have affinity for non-human analogues the Ag too low to be of any use
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                Length 121;
                                                                                                                                                                                     tch 100.0%; Score 649; DB 2; Length 1: al Similarity 100.0%; Pred. No. 1.7e-49; 121; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhesusised antibody mutant heavy chain SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY82348 standard; protein; 121 AA.
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                                                                                                                       Sequence 121 AA;
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to active anticancer agent, and (v) for affinity chromatography. The Abretain about the same activity in adheaion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine anti-CD11a antibody MHMZ4 has IC50 0.09 mM for preventing adheaion between Jurkat cells (expressing LFA-1) and normal epidermal keratinocytes that express ICAM-1 (intracellular adhesion molecule-1). The fully humanized version of MHMZ4 had IC50 0.13 nM. The present sequence represents the amino acid sequence of a rhesusised antibody mutant heavy chain, which is used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; CD11a; I-domain; monoclonal antibody; cluster of differentiation 11a; mixed lymphocyte response assay; Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule; ICAM-1; lymphocyte function-associated antigen 1 mediated disorder; psoriasis; Crohi's disease; ulcerative colitis; dermatitis; asthma; rhemmatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; prodrug activating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanized anti-CD11a antibody useful for treating lymphocyte function-
associated antigen mediated disorder e.g. psoriasis, Crohns disease,
ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKDRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                                                  EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWYGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS
                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                                                                                                                                                                                                                     100.0%; Score 649; DB 3; Length 121; 100.0%; Pred. No. 1.7e-49; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhesusised mouse anti-CD11a I-domain antibody VL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG39012 standard; protein; 121 AA.
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97US-00974899.
99US-00420745.
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                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                      Sequence 121 AA;
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20-NOV-1997;
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(CD) 11a antibody having specificity to human CD11a 1-domain or CD11a with a kd value of not more than 1x10-8 M, or concentration for 50 f inhibition (ICSO) (nM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing addression of Jurkat cells to normal human cupidermal keratinocytes expressing intercellular adhesion molecule (ICAM) -1. Also included area kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The antibody is useful for determining the presence of CD1a protein and for treating lymphocyte function-associated antigen | mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, sathma, creating arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mallitus. The antibody is useful when conjugated to a condidabetes multipody so a sathma, creating enzyme, or as an affinity purification agent. The present sequence is the light chain of a rhesusised ant-CD11a antibody of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adult respiratory discress syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SLE; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis; orbo, CNS inflammatory disease; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak; scal malignancy; chronic lymphocytic lenkaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; murine anti-human CDlia monoclonal antibody; MEM24; variable heavy chain; WH; murine; rhesus macaque; fusion protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKORFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD11a antibody, human immunodeficiency virus infection, HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BUQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHWMWWRQAPGKGLEWVGMIAPASSSTRY
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invention relates to a Humanised anti-cluster of differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhinovirus infection; inflammatory skin disease; psoriasis;
inflammatory bowel disease; Crohn's disease; ulcerative colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhesusised MHM24 antibody variable heavy chain mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 649; DB 8;
100.0%; Pred. No. 1.7e-49;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             the invention.
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AAW63532 standard; protein; 121 AA.
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                                     97WO-US019041.
                                                                       96US-00757205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 96.7
Matches 117; Conservative
                                                                                                                                             Jardieu PM, Presta LG;
                                                                                                         (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukaemia, etc
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                                     20-OCT-1997;
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 04-JUN-1998
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                                                                                                                                                                                                                                                                                 The present interaction retactes to an autonouy micention is a special dependent antibody with beneficial properties. The invention is useful for treating and preventing infectious diseases such as human immunosity in thinovitus infections, infilammatory skin disease such as paoriasis, inflammatory bowel diseases such as Crohn's disease such as paoriasis, inflammatory bowel diseases such as Crohn's allergic diseases such as exceed and asthma, autofmnume diseases such as the municipal diseases such as profits, systemic lupus erythmatosus (SLB), diabetes cuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is rhesualsed murine anti-human CDla monoclonal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                          New antibody mutant of a species-dependent antibody, useful for thand preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
                                                                                                                                                                                                                                                                       The present invention relates to an antibody mutant of a species-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity determining region; heavy chain variable region; humanised antibody; MHM24F(ab)-8; anti-CDlla antibody; human CDlla I domain; MHM24 epitope; alpha subunit; lymphocyte function-associated antigen 1; LFA-1; immunoassay; in vivo imaging; diagnosis; CDlla-associated disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 649; DB 8; Length 121; 100.0%; Pred. No. 1.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy chain variable region of humanised anti-CD11a antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                 Example; SEQ ID NO 17; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW62013 standard; peptide; 121 AA.
                  97US-00975329
 96US-0031945P
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Matches 121; Conservative
                                                                                      Jardieu PM, Presta LG
                                                  (GETH ) GENENTECH INC.
                                                                                                                          WPI; 2004-552640/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 121 AA;
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27-NOV-1996;
                20-NOV-1997;
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The present sequence represents the heavy chain variable region of a humanised anti-CDI1a antibody that binds specifically to the human CDI1a I domain (MHM24 epitope). CDI1a refers to the alpha subunit of lymphocyte function-associated antigen I (LPA-1) from any mammal. The humanised anti-CDI1a antibodies are used to determine presence of CDI1a in usual associated by in vivo imaging, particularly for diagnosis of CDI1a associated diseases (typically immune responses and inflammation such as portasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.4%; Score 632; DB 2; 96.7%; Pred. No. 5.4e-48;
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and was used to produce a mutant of the invention. The mutants are of a species-dependent antibody (Ab), and have an amino acid substitution in a variable region of the Ab, and binding affinity for an antigen (Ag) from a non-human mammal at least 10 times stronger than for the wild type Ab against the Ag. The mutant antibodies are particularly intended for administration to a non-human mammal in preclinical studies (e.g. of infection, immunity, haematopolesis or transplantation). They can also be used diagnostically (to identify specific proteins) or therapeutically, e.g. where directed against CDIIa (Iymphocyte function-associated antigen 1) or intercellular adhesion molecule-1 against a wide variety of inflammatory or autoimmune diseases, malignancies, transplant rejection, human immune deficiency wirus infection and tumour cell invasion. Conversion to the mutant form allows useful antibodies to be produced from antibodies which normally have affinity for non-human analogues of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the heavy chain of the humanised antibody MHM24,
                                                                                                                                                                                     Mutants of species-dependent antibodies with affinity for non-human mammalian antigen - greater than for parent antibody, particularly used for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies directed against CD1a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.4%; Score 632; DB 2; Length 121; Best Local Similarity 96.7%; Pred. No. 5.4e-48; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 55; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Ag too low to be of any use
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                                     Presta LG;
                                                                                                                 WPI; 1998-322726/28
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                                 Jardieu PM,
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The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosupressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated with inflammatory and involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (1) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen-I (LFA-1; CD11a) (-9. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs to active anticancer agent; and (v) for affinity chromatography. The Ab cream activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion between Jurkat cells (expressing LFA-1) and normal epidermal charter antibody when the tracellular adhesion molecule-I). The fully humanized version of MHM-1 (intracellular adhesion molecule-I). The fully humanized version of MHM-1 (anticacllular adhesion molecule-I).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                    New humanized anti-CD11a antibody, useful for treating or preventing e.g. inflammation and transplant rejection, contains human heavy variable
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                                                                                                                                                                                                              region complementarity determining regions.
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96US-0031971P.
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Matches 117; Conservative
                                                                                  Jardieu PM, Presta LG
                                        (GETH ) GENENTECH INC.
                                                                                                                            WPI; 2000-282241/24.
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27-NOV-1996;
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C(D) lia antibody having specificity to human CD11a I-domain or CD11a with a kd value of not more than 1x10-8 M, or concentration for 50 % inhibition (ICSO) (IM) value of not more than 1 mM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM) of the following the antibody and instructions for use to detect the CD11a protein, an isolated mucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising cantibody, a vector comprising the nucleic acid, a host cell comprising cantibody is expressed. The antibody by culturing the cell so that the antibody binds to epitope MHM24 on CD11a. The antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The antibody is aspected antibody by culturing the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such as psoriasis, Crohn's alsesse, ulcerative colitis, dermatitis, asthma, cheumatoid arthritis, systemic luque erythematoeus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The mouse anti-CD11a I domain monoclonal antibody MHM24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                        Humanized anti-CD11a antibody useful for treating lymphocyte function-
associated antigen mediated disorder e.g. psoriasis, Crohns disease,
ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a Humanised anti-cluster of differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.4%; Score 632; DB 8; Length 121; 96.7%; Pred. No. 5.4e-48; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 5; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR03368 standard; protein; 121 AA
                                                                                                                                                                           96US-0031971P.
97US-00974899.
99US-00420745.
                                                                                                                                    28-FEB-2001; 2001US-00795798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.77
Matches 117; Conservative
                                                                                                                                                                                                                                                                                             Jardieu PM, Presta LG;
                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                         US2003207336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121 AA;
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20-NOV-1997;
                                                                                                                                                                                                                    20-OCT-1999;
                                                                                               06-NOV-2003
Synthetic.
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                    Mus sp.
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The present invention relates to an antibody mutant of a species—
dependent antibody with beneficial properties. The invention is useful
for treating and preventing infectious diseases such as human
immunodeficiency virus (HIV) and rihinovirus infections, inflammatory skin
disease such as psoriasis, inflammatory bowel diseases such as Crohn's
disease and ulcrative colitis, adult respiratory distress syndrome,
allergic diseases such as eczema and asthma, autoimmune diseases such as
rheumatoid arthritis, systemic lupus erythematosus (SLB), diabetes
rheumatoid arthritis, polymyositis and chronic obstructive pulmonary
disease (COPD), CNS inflammatory disorder, skin hypersensitivity
disorders such as poison ivy and poison oak, B-cell malignancies such as
chronic lymphocytic leuksemia and hairy cell leukaemia, graft versus host
disease and cancer. The invention is also useful in gene therapy. The
present sequence is humanised murine anti-human CDlia monoclonal antibody
                                     rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; adult respiratory distrass syndrome; allergic disease; eczema; asthma; autolummune disease; rheumatoid arthritis; systemic lupus erythematosus; SiB; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; polson ivy; poison oak; slaidynancy, chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; murine anti-human CDIIa monoclonal antibody; MHM24; variable heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibody mutant of a species-dependent antibody, useful for treating and preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MHM24) F(ab)-8 variable heavy chain protein. This sequence is used in
                     CD11a antibody; human immunodeficiency virus infection; HIV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the exemplification of the invention.
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                                                                                                                                                                                                                                                                                            7H; murine; human; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-2003; 2003US-00727737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0031945P.
97US-00975329.
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Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jardieu PM, Presta LG;
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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20-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                     Chimeric.
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셤
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121 S 121

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Humanised MHM24 F(ab)-8 antibody variable heavy chain protein.

(first entry)

21-OCT-2004

121 \$ 121

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61 NOKPKDRFTISVDKSKNTLYLØMNSLRAEDTAVYYCARGIYFYGTTYFDYWGGGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a recombinant monoclonal antibody for human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID No.5 in light-chain variable region and the amino acid sequence shown by SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its bioactivity and the expression in host cell are greatly increased. The DNA molecule for coding the antibody, its preparation process and the medicinal composition containing it are also disclosed. The present sequence represnts a heavy chain variable region of human CD11a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWNNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant human CD11a monoclonal antibody and its preparation and
                                                                                                                                          monoclonal antibody; CD11a; light-chain variable region; heavy-chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 632; DB 8;
Pred. No. 5.4e-48;
1; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                 (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
                                                                                                                   CD11a heavy chain variable region #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADX80646 standard; protein; 121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 14-15; 16pp; Chinese.
                           ADW38458 standard; protein; 121 AA.
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Best Local Similarity 96.7%;
Matches 117; Conservative 1
                                                                                                                                                                                                                                                                                      20-FEB-2002; 2002CN-00110866.
                                                                                                                                                                                                                                                                                                                     20-FEB-2002; 2002CN-00110866
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            medicinal composition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 121 AA;
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                                                                                                                                                                                               Homo sapiens
                                                                                       24-MAR-2005
                                                                                                                                                                                                                            CN1439651-A
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                                                           ADW38458;
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RESULT 11
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                 ADW38458
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The invention relates to a method of purifying a protein which comprises C a CH2/CH3 region by protein A affinity chromatography. The method involves reducing the temperature of a composition comprising the protein and one or more impurities subjected to protein A affinity chromatography c to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably the protein is antibody. The antibody is selected from Trastuzumab, chmanized 2C4, humanized CD11a antibody, and humanized VEGF antibody. Preferably, the antibody binds HRZ antigen, where the antibody is C Trastuzumab or humanized 2C4. The protein is an immunoadhesin, C Trastuzumab or humanized 2C4. The protein is an immunoadhesin, and specifically a TNF receptor immunoadhesin. The methods are useful for specifically a TNF receptor immunoadhesin. The methods are useful for affinity chromatography and for reducing leaching of protein A during c protein A affinity chromatography. The current sequence represents the coverable heavy chain amino acid sequence of CD11a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKEKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKPKORPTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTIYFDYWGQGTLVTVS 120
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                                         Protein purification; leaching; protein A affinity chromatography; CD11a;
                                                                                                                                                                                                                                                                                                                                                                                comprises reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWANWVRQAPGKGLEWVGMIAPASSSTRY
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                                                                                                                                                                                                                                                                                                                                                                              Purifying a protein, e.g. antibody or immunoadhesin, comprises reducir the temperature of a composition subjected to protein A affinity chromatography to 3-20 degrees C, where protein A leaching is reduced.
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         Humanized CD11a variable heavy chain amino acid sequence, seq id
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purifying; target protein; non-affinity purification;
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Pred. No. 5.4e-48;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                               Mcdonald PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6; 27pp; English.
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Best Local Similarity 96.7%;
Matches 117; Conservative
                                                                                                                                                                                                        24-JUN-2004; 2004US-00877532.
                                                                                                                                                                                                                                          28-JUL-2003; 2003US-0490500P
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                                                                                                                                                                                                                                                                                                                 Laverdiere
                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-172327/18.
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                                                                                                                                       US2005038231-A1.
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                                                                                                                                                                         17-FEB-2005
                                                                                                                                                                                                                                                                                                                  Fahrner RL,
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                                                                                                     Synthetic
                                                                  antibody
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0; Gaps

Length 121 3; Indels 9 9

(first entry)

05-MAY-2005

ADX80646;

fusion protein. Homo sapiens.

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The invention relates to a method for purifying a target protein from a mixture containing a host cell protein. This method comprises subjecting the mixture to a non-affinity purification followed by high-performance tangential flow filtration (HPTPP) and isolating the protein in a purity containing less than 100 parts/million (ppm) of the host cell protein, where the method of the invention includes no affinity purification, process. The method of the invention is useful for purifying a target protein from a mixture containing a host cell protein, and is useful for incorporating the isolated protein into a pharmaceutical formulation. Proteins purified using the method of the invention are useful in a pharmaceutical respect, and are also useful in various diagnostic and therepeutic purposes. The method of the invention is efficient in the argument protein from a mixture containing a host cell protein, and may also be effectively performed at low cost. The current sequence. This represents the anti-CDIIa rhuMAb heavy chain amino acid sequence. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particular protein was used to demonstrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                          Purifying target protein from mixture containing host cell protein involves subjecting mixture to non-affinity purification, high-performance tangential flow filtration and isolating purified protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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tangential flow filtration; HPTFF; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8; diagnosis; inflammatory disorder; conjugate; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.4%; Score 632; DB 8; Length 451; larity 96.7%; Pred. No. 2.1e-47; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human IgGl subgroup III heavy chain variable domain.
                                                                                                                                                                                                                                                                                                  Van Reis R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 4; 77pp; English
                                                                                                                                                                                                                                                                                                  Lebreton B,
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                    diagnostic, therapeutic, antibody
                                                                                                                                                                             25-APR-2003; 2003WO-US013054.
                                                                                                                                                                                                                    26-APR-2002; 2002US-0375953P
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                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
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  high-performance
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antibody fragments covalently attached to one or more nonprotestinated polymer molecules, where the apparent size of the conjugate is at least about 500 kba. Conjugates of antibody fragments which bind the human interleukin (IL) 8 with a nomprotestinaceous polymer can be used for treating inflammatory disorders e.g. acute lung injury, ischaemic reperfusion disorder, and autoimmune diseases. They can also be used for treating e.g. inflammatory skin diseases including psoriasis and atopic dermatitis, systemic scleroderm and sclerosis, and asthmatic diseases. The conjugates can also be used as reagents in an animal model system for in vivo study of the biological functions of the antigen recognised by the conjugate. The present sequence represent the human IgG1 subgroup III heavy chain variable domain form the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.5V11N35A; inflammatory disorder; adult respiratory distress syndrome; chimeric; affinity purification; 6G4.2.5.
                                                                                                                                                                                                                                                                                                                                                           conjugates of nonproteinaceous polymers with antibody fragments, used treating inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BVQLVESGGGLVQPGGSLRLSCAASGFSFTGHWMWWVRQAPGKGLEWVGMIHPSDSETRY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes a novel conjugate having one or more
                                                                                                                                                                                                                                                                                         Zapata GA;
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                                                                                                                                                                                                                                                                                         Shahrokh
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                                                                                                                                                                                                                                                                                         Leong SJ, Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 29; 360pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY77755 standard; protein; 116 AA
                                                                                                                                                                                                    98US-00121952.
98US-00122513.
                                                                                                                                   99WO-US001081.
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98WO-US003337.
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Best Local Similarity
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                                                                 W09937779-A1
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98US-00027449.
              97US-0038664P.
98US-0074330P.
                                Presta LG, Leong SR,
                         (GETH ) GENENTECH INC.
                                       WPI; 2000-181809/16.
       20-FEB-1998;
              21-FEB-1997;
22-JAN-1998;
15-FBB-2000
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Gonzalez TN;

The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 (G4.2.5V1N35A light chain; and amino acids 24-253 of the humanized anti-IL-8 (G4.2.5V1N35A heavy chain. The anti-IL-8 MAbs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-IL-8 MAb can be associated in a vector with another gene encoding another protein or protein fragment to produce a fusion protein which can make isolation and/or purification of the protein an New nucleic acid molecule encodes a polypeptide which is an anti-interleukin-8 monoclonal antibody or antibody fragment useful for the production of anti-interleukin-8 monoclonal antibodies or fragments. Example, Fig 29, 188pp, English.

Sequence 116 AA;

1; Gaps Query Match

84.5%; Score 548.5; DB 3; Length 116;
Best Local Similarity 88.8%; Pred. No. 1.2e-40;
Matches 103; Conservative 2; Mismatches 10; Indels 1

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Ig heavy chain V r
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Length 125 19; Indels

71.0%; Score 461; DB 2; 72.0%; Pred. No. 5.6e-36; ive 12; Mismatches 19

Query Match Best Local Similarity 72.09 Matches 90; Conservative

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1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWYRQAFGKGLEWISYISSSSSTIYY EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY

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A;Cross-references: UNIPARC:UPI0000116477; EMBL:214205; NID:930969; PIDN:CAA78574.1; PID: C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

A; Accession: S31686 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-140 <CUI>

C;Speciés: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S1686
E;Accession: S1686
E;Culsinier, A.M., Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585

S31686 Ig heavy chain V region - human (fragment)

Ig heavy chain V r Ig heavy chain I r Ig heavy chain V r Ig heavy chain I r	ALIGNMENTS S10531 19 heavy chain V region - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Accession: 830531 R;Mariette, X. R;Mariette, X. R;Mariette, X. A;Maceronce number: 830520 A;Accession: 830531 A;Accession: 830531 A;Accession: 830531 A;Accession: 830531 A;Accession: 830531 A;Accession: 830531 A;Accession: Byceliminary A;Acc
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 S30531 Ig heavy chain V region - human C; Species: Homo sapiens (man) C; Species: 06-Jan-1995 #sequence_revision 06-Jan C; Accession: S30531 R; Mariette, X. submitted to the EMBL Data Library, October 1 A; Reference number: S30520 A; Accession: S30531 A; Residues: 1-125 AMAR> A; Residues: 1-125 AMAR> C; Superfamily: immunoglobulin homology C; Superfamily: immunoglobulin F; 15-98/Domain: immunoglobulin homology <ifwm></ifwm>
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Matches 89; Conserv
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A;Molecule type: mRNA
A;Residues: 1-128 <MOR>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI0000116472; EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;34-117/Domain: immunoglobulin homology <IMM>
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R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31588
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R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of shacesence number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
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IG heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo Bapiens (man)
C;Date: 24-Uul-1998 #Bequence_revision 24-Jul-1998 #text_change 31-Dec-2004
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                    20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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                                                 / Match 71.0%; Score 461; DB 2; Length 140; Local Similarity 73.6%; Pred. No. 6.3e-36; Lonservative 12; Mismatches 20; Indels
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C;Superfamily: immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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F;34-117/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-140 <CUI>
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C'Speciés: Homo sapiens (man)
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C'Accession: S26786
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J. Immunol. 22, 241-245, 1992
Bur. J. Immunol. 22, 241-245, 1992
A;Fitle: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene famil
A;Reference number: S26786; MUID:92111632; PMID:1730251
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C;Species: Homo sapiens (man)
C;Accession: S26798
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Bur. J Immunol. 22, 241-245, 1995
A;Fitle: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene famil
A;Reference number: S26786; MUID:92111632; PMID:1730251
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 - MOR>
A;Cross-references: UNIPARC:UPI0000115FC6; EMBL:X61015; NID:932795; PIDN:CAA43349.1; PID: C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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       Length 140,
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                                                                    22; Indels
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ch 70.7%; Score 459; DB 2; Similarity 73.6%; Pred. No. 9.6e-36; 89; Conservative 10; Mismatches 22.
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Matches 87; Conservative
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C;Accession: S23624
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; (
J. Exp. Med. 175, 831.842. 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv
A;Reference number: S23623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI0001163EA; EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C_Species: Joreb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: $20782
R;Mortari, F.; Wang, J.; Schroeder, H.W.
R;Mortari, F.; Wang, J.; Schroeder, H.W.
A;Description: Analysis of the IgA and IgG rearranged VH repertoire of human cord blood A;Reference number: $20765
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                               1 EVQLIBSGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY
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     Length 119;
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Score 454; DB 2;
Pred. No. 2.4e-35;
9; Mismatches 20,
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%; Pred. No. 3.4e-35;
11; Mismatches 20,
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  70.0%;
74.4%;
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72.6%;
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Best Local Similarity 72.64
                                                            Conservative
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A,Molecule type: DNA
A,Residues: 1-124 <MOR>
                               Local Similarity
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C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar Bur. J Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H) 3 genes and short diverse third complem A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: S31107
R;Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman Bur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem A;Reference number: S31104; WUID:92111633; PMID:1730252
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A., Residues: 1-119 <RAA>
A., Cross-references: UNIPARC:UPI0000176DC7; EMBL:X62955
A., Cross-references: UNIPARC:UPI0000176DC7; EMBL:X62955
A., Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C.; Superfamily: immunoglobulin V region; immunoglobulin homology
C.; Keywords: heterotetramer; immunoglobulin homology <IMM>
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A)Cross-references: UNIPARC:UPI0000176DCB; EMBL:X62956
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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  Similarity 71.9%; Pred. No. 1.3e-35; 87; Conservative 7; Mismatches 27;
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Pred. No. 1.9e-35;
9; Mismatches 17
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Local Similarity 74.0%;
nes 91; Conservative
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Ig heavy chain - human
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Ig heavy chain V region (VH3DJH4) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000 C;Accession: S1966 R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.Mol. 801, 222, 581-597, 1991 A;Fille: By-passing immunization. Human antibodies from V-gene libraries displayed on pht A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UP10000116701; EMBL:246382; NID:9562324; PIDN:CAA86521.1; PII CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S48798
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48797
A;Reference number: S48797
A;Reference number: S48798
A;Status: preliminary
                                                                                                                                                                     61 NOKFKORFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYF--DYWGOGTLVT 118
                                                                                                                                                                                                 61 ADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARSIKYYDENYYGMDVWGQGTTVT 120
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                                                                                        1 EVOLVESGGGLVQPGGSLRLSCAASGFTFSSYSMWVRQAPGKGLEWVSYISSSSSTIYY
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  22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - human
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  11; Mismatches
  88; Conservative
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A; Residues: 1-120 < MAH>
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A; Residues: 1-121 < MAR>
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C,Accession: S26794

Newton, 0.7., Wang, J.Y.; Schroeder Jr., H.W.

Eur. J. Immunol. 22, 241-245, 1992

A,Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family. Reference number: S26786; MUID:92111632; PMID:1730251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC:UP1000011647C; EMBL:Z14212; NID:g30959; PIDN:CAA78581.1; PIL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C'Species: Homo sapiens (man)

C'Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C'Accession: 831669

R'Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

Bubmitted to the EMBL Data Library, June 1992

A; Description: Mechanisms that generate human immunoglobulin diversity operate from the
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                                                                                                                                                                                           61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYSMNWYRQAPGKGLEWYSYISSSSSTIYY
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; Pred. No. 6e-35;
11; Mismatches 21; Indels 1
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Pred. No. 5.8e-35;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <!MM>
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74.4%; Pred. No. 5.5e-35;
tive 9; Mismatches 18;
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Best Local Similarity 73.0%;
Matches 89; Conservative 1
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                            90; Conservative
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <CUI>
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A,Status: preliminary
A,Molecule type: mRNA
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RESULT 15
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19 heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31587
R;Culainier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
R;Description: Mechanisms that generate human immunoglobulin diversity operate from the A;Reference number: S31585
A;Accession: S31587
A;Accession: S31587
A;Accession: Syles
A;Retriumnary
A;Residense: 1-136 <CUI>

k,Cross-references: UNIPARC:UPI0000116468; EMBL:Z14189; NID:931005; PIDN:CAA78558.1; PID C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;31-114/Domain: immunoglobulin homology <1MM>

9 1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 69.0%; Score 447.5; DB 2; Length 136; 72.7%; Pred. No. 1.1e-34; tive 9; Mismatches 23; Indels 1; Gaps Query Match
Best Local Similarity 72.7%
Matches 88; Conservative

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Search completed: April 13, 2006, 17:19:34 Job time : 27.8908 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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09UL91_HUMAN
HV39_MOUSE
06MZU6_HUMAN
09UL72_HUMAN
08UUX1_HUMAN
09UL88_HUMAN
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Q6MZV7_HUMAN
Q65ZC9_HUMAN
Q96K68_HUMAN
HV07_MOUSE
Q924Q7_MOUSE
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HV41 MOUSE
QSBK12 RAT
Q6MZQ6 HUMAN
Q924Q3 MOUSE
Q6N089 HUMAN
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Q96BB9_HUMAN
QGGMYZ_HUMAN
Q4VBH1_RAT
HV38_MÖUSE
Q5PQK9_RAT
Q6PJA4_HUMAN
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Q6P181_HUMAN
HV40_MÕUSE
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Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot;*
2: uniprot_trembl:*
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Result

Q9u193 homo sapien Q4v9z4 mus musculu Q504m7 mus musculu Q6n096 homo sapien Q51218 mus musculu Q9z4r8 mus musculu Q9y509 homo sapien Q6xvX0 homo sapien Q6xvX0 homo sapien Q8vu38 homo sapien Q9z4r3 mus musculu P01812 mus musculu Q6mzx9 homo sapien Q6xx9 homo sapien Q8xx19 homo sapien Q8xx19 homo sapien Q8xx19 homo sapien Q8xx29 homo sapien Q6mzx9 homo sapien	ALIGNMENTS T. 1 WOUSE HV37 WOUSE FRANDARD; PRT; 119 AA. 12-3UL-1986 (Rel. 01, Last sequence update) 13-5EP-2005 (Rel. 94, Last sequence update) 13-5EP-2005 (Rel. 94, Last amnotation update) 14-5EP-2005 (Rel. 94, Last amnotation update) 14-5EP-2005 (Rel. 94, Last amnotation update) 15-5EP-2005 (Rel. 94, Last amnotation update) 15-5EP-2005 (Rel. 94, Last amnotation update) 16-1 16-1 16-1 16-1 16-1 16-1 16-1 16-	.n; ; CRC64;
2 Q9UL93 HUMAN 2 Q4V924 MOUSE 2 Q504M7 MOUSE 2 Q504M7 MOUSE 2 Q504M7 MOUSE 2 Q5F2IB MOUSE 2 Q5F2IB MOUSE 2 Q9Y509 HUMAN 2 Q5F2IB MOUSE 2 Q9Y509 HUMAN 2 Q6TX09 HUMAN 2 Q6TX0 HUMAN 2 Q62XX0 HUMAN 2 Q924R3 MOUSE 1 HV42 MOUSE	ALIGNMENTS TO WOUSE PUNDS PUNDS PUNDS PUNDS PUNDS PUNDS 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 13-SEP-2005 (Rel. 18, Last annotation update) Mus musculus (Mouse) Eukaryota, Metazoa, Chordata, Cramiata, Vertebrata; Buteleostomi; Musmalia, Butheria, Buarchontoglires; Glires; Rodentia; Sciurogna Murcidae, Muridae, Musinae; Mus. PROFIE BALLANDS (1) PROFIE SQUENCE RAD D.N. Radikoff S., Krutzach H., Potter M.; Rodentia; Sciurogna Murcidae, Muridae; Mus. (1) PROFILINS -79223895; PubMed=111245; RAD D.N. Radikoff S., Krutzach H., Potter M.; Proc. Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins a its potential role in generating diversity in complementarity-determining regions.; U.S.A. 76:2890-2894(1979). Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979). NUCLECTIDE SEQUENCE OF 1-118. MIDITAR A. III Glasel J. A. 78(1989). "Comparative sequence and immunochemical analyses of murine monoc anti-morphine anti-morphine and immunochemical role in generative sequence and immunochemical role in the comparative sequence and immunochemical role in the role in Sequence and immunochemical r	; 1. ; Immunoglobulin domain; Ig-like. MW; BC34FC8F31CD41B3 CRC64;
64.1 64.1 116.6 63.3 63.3 63.3 63.3 63.3 63.3 6	MUSE MUSE HV37 MOUSE STANDARD; PRT; P01807; 21-UUL-1986 (Rel. 01, Last sequence 13-SEP-2005 (Rel. 49, Last annotati 14 heavy chain V region X4. Museullus Eutheria; Buarchontcoglire Murcidae; Murinae; Mus. NCBI TaxID=10090; RAO D.N., Rudikoff S., Krutzech H., Structural evidence for independer 1mmunoglobulin heavy chains from art 1sts potential role in generating di 4ctermining regions."; Proc. Natl. Acad. Sci. U.S.A. 76:28 NUCLSON NATL. Acad. Sci. U.S.A. 76:28 ACCOMPARATIVE SEQUENCE OF 1-118 MEDLINE=90064331; PubMed=2555519; MILLER A. III, Glasel J.A.; J. Mol. Biol. 209:763-778(1999). - MISCELLANEOUS: This chain was it that binds galactan. - SIMILARITY: Contains I Ig-like - SIMILARITY: SWOWNGSOO000003483; Mus mm InterPro; IPRO031596; Ig-V. SWART; SWOWNGSOO00000349; Mus mm InterPro; IPRO03169; IG-V.	50835; IG_LIKE; 1. ein sequencing; Imm lin V region. 1 117 117 119 119 119 AA; 13246 MW;
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	RESULT 1 19 31 - 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

DB 1; Length 119;

68.2%; Score 442.5;

Query Match

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Name=IGHM;
                 Query Match
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Colline F.S., Wagner L., Shaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A statchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Statchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahesley J., Helton E., Ketreman M., Madan A.M., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Redersation and initial analysis of more than 15,000 full-length human
                7
                                                                                                        61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAR-LHYYG--YAAYWGQGTLVTVS 117
                                                                                         61 NOKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                 9
                                                    1 EVKLLESGGGLVQPGGSLKLSCAASGPDFSRYWMSWYRQAPGKGLEWIGEINPDSSTINY
                                                                                                                                                                                                                                                                                                                                          Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                       1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                3; Gaps
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RMBL; BC073771; AAH73771.1; -; mRNA.

SMR; QGGMX2; 263-471.

InterPro; IPR007599; IG.

InterPro; IPR007599; IG.

InterPro; IPR003599; IG.

InterPro; IPR003599; IG.

InterPro; IPR003596; IG.

RINERPRo; IPR00356; IG.

RMAT; SM00409; IG.

RMAT; SM00409; IG.

RSMART; SM00409; IG.

RPC0SITE; PS56983; IG.

RRC0SITE; PS68939; IG.

RRC0SITE; PS68939; IG.

RRC0SITE; PS68039; IG.

RRC0SITE; PS68939305B286203 CRC64;
 67.8%; Pred. No. 3e-39;
tive 19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                       PRT;
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             82; Conservative
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Best Local Similarity
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Name=IGHAl;
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MEDLINE-22388257; PubMede-12477932; DOI=10.1073/pnas.242603899;

MEDLINE-228825. L. Handellar G.M., Schaefer C.F., Bhat N.K.,

MEDLINE R.P., Jordan H., Moore T., Max S.I., Wann J., Haieh F.,

MEDLINE R.P., Jordan H., Moore T., Max S.I., Wann J., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MEDLINE S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

MEDLINE S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

MILALON D.K., Muzny D.M., Sodergren B.J., Lu X., Ginbaratne P.H.,

Millahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Millahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Milling M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Millahon D.K., Millahon J.W., Green B.D., Dickson M.C.,

Makeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Makeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Makeeley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                        61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGOGTLVTVS 120
                                                                                                                                                                                                                                                                                                                              80 ADSVKGRPTISRDNAKNTLYLQMNSLRGEDAAVYYCARGFVSLPRSTLDIWGQGTWVTVS 139
                                                                                                                                                                                       20 EVQLVESGGGLVQPGGSLRLSCAASGFIFSSYWMHWVRQAPGKGLVWVSRINSDGSSTSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
PubMed=2500644;
Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
"Nucleotide sequences of the CDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                          Gaps
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       Length 493;
                                                                       28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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   , DB 2;
1.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 AA.
68.1%; Score 442; DB 71.1%; Pred. No. 1.8e. ive 7; Mismatches
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EMBL; BCOL5760; AAH15760.1; -; mRNA.
PIR; SO5271; SO5271.
PIR; S24260; S24260.
HSSP; P01861; 1ADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Q96BB9;
                                 Local Similarity 71.19
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Q6GMY2; 20-256
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NIH MGC Project;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Detchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B. Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B. Rownstein M.J., McKernan K.J., Moramson R.D., Mullahy S.J.,

B. Bosak S.A., McEwan P.C., Abremon R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.B.,

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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                  61 NQKFXDRFTISVDXSKNTLYLQMNSLRAEDTAVYYCA---RGIYFYGT-TYFDYWGQGTL 116
                                                                                                                                                                                                                                                                                                  80 ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL 139
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                           20 EVQLIESGGGLVQPGGSLRLSCAASGFSFSSYAMWWVRQAPGKGLEWVSAISGSGGSTYY
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                  4,
                                                                                                                                                                   68.1%; Score 442; DB 2; Length 597; 72.8%; Pred. No. 2.2e-38; ive 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH MGC Project,
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073758; AAH73758.1; -; mRNA.
                                                                                                                                       597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
           InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig-21.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003506; Ig_MHC.
Pfan; PR07554; CI-8et; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Ensembl; ENSG0000130076; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       QGGMY2_HUMAN PRELIMINARY;
                                                                                                                                                                                Local Similarity 72.8
nes 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
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                                                                                                                          Immunoglobulin domain.
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                                                                                                                                       SEQUENCE
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Rausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A pischel S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A pischenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Brownstein M.J., Wakernan K.J., Mahak J.A., Gunstene P.H.,
Broak S.A., McKwan P.J., McKernan R.J., Mahak J.A., Gunstene P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Sharochenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzzywinski M.I., Skalska U., Smailus D.E.,
Broherzetion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARG--------IYFYG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 QVQLVBSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Mētazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 606;
INTERPRO, IRRO07110; Ig-like.
INTERPRO, IRRO07110; Ig-like.
INTERPRO, IRRO03006; Ig-like.
INTERPRO, IRRO03006; Ig-MC.
INTERPRO, IRRO03006; Ig-MHC.
INTERPRO, IRRO0409; Ig-V.
INTERPRO, IRRO0409; IG-V.
INTERPRO, IRRO0409; IG-V.
INTERPRO, IRRO-V.
INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Indels
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 68.0%; Score 441.5; DB 2
1 Similarity 63.5%; Pred. No. 2.6e-38;
87; Conservative 14; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 ---MDVWGQGTTVTVSS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4VBH1_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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Name=LOC299354;
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121 8 121
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Name=Igha;
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SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTY-FDYWGQGTLVTV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 PDSVKGRFTISRDNAENTVYLQMNSLRSEDTATYYCAKGGEYYGYNYPFDYWGQGVMVTV 139
                                                                                                                                                                                                                                                                                                                                                                                                  20 EVQLVETGGGLVQPGRSLKLSCVASGFTFSSYWMYWIRQAPGKGLEWVSSINTDGGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                             1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rao D.N., Rudikoff S., Krutzach H., Potter M., Structural evidence for independent joining region gene in "Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions ", Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).

-I-MISCELLANEOUS: This chain was isolated from an IGA myeloma protein that binds galactan.
            C -1 - FUNCTION: Beca-2-microglobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).

-1 - SUBCELLULAR LOCATION: Secreted (By similarity).

R EMBL; BC058846; AAH95846.1; -; mRNA.

R InterPro; IPR001599; Ig.

R InterPro; IPR001599; Ig.

R InterPro; IPR001599; Ig.

R Pfam; PR0764; C1-set; 3.

SMART; SM00409; IG; 2.

R RAART; SM00409; IG; 2.

R RAART; SM00406; IGv; 1.

R RAART; SM00406; IGv; 1.

R PROSITE; PS50835; IG LIKE; 4.

M Immunoglobulin domain; Repeat.

SEQUENCE 467 AA; 51651 MW; IPP0328F50160ED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                        DB 2; Length 467;
                                                                                                                                                                                                                                                                                                     67.6%; Score 438.5; DB 2; Length 67.2%; Pred. No. 4e-38; ative 14; Mismatches 25; Indels
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A02078; AVMST6.
HSSP: P01810; 2FBJ.
SMR; P01810; 1-119.
Ensembl; ENSMUSG0000003483; Mus musculus.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007596; Ig-v.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-79223895; PubMed=111245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region T601.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                        82; Conservative
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN SEQUENCE.
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P01808;
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MEDLINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jornathan H., Moore T., Max S.I., Wang J., Heisteh F., Stapleton M., Sarese M.B., Ponaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Uedin T.B., Toshiyuti S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H., Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Allahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Makeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Ablacebey R.W., Touchman J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Machara M.A., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                        61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCAR-LGYYG--YFDVWGAGTTVTVS 117
                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butcharia; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                     3; Gaps
                                                                                                                                                       ch 67.4%; Score 437.5; DB 1; Length 119; Similarity 67.8%; Pred. No. 1e-38; 82; Conservative 17; Mismatches 19; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC087137; AAH87137.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                           119 119 119 119 MW; BC38CC84E6EA00E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
1 112 IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG_C1.
InterPro; IPR003006; IG_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEPOK9 RAT PRELIMINARY,
OSPOK9,
01-PEB-2005 (TrEMBLrel. 29
01-PEB-2005 (TrEMBLrel. 29
01-PEB-2005 (TrEMBLrel. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
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IPR007110;
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                                                                                                                                                                                                                                                                                                 Query Match
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DD 7 10-M

DD 7 10-M

DD 1 10-M

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X Straubberg R.L., Person B.C., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wardner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

D. Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

B tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

B stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Iu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

B Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       80 PDSVKGRFTISRDNAKSTLYLQMNSLRSEDTATYYCTRAAHVMGPYYFAYWGQGVMVTVS 139
                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                          1 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                        67.2%; Score 436; DB 2; Length 479; 66.9%; Pred. No. 7.6e-38; ive 9; Mismatches 31; Indels
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Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO18747; AAH18747.1; -; mRNA.
HSSP; P01861; IADQ.
                                    Pfam; PP07654; C1-set; Z.
SMART; SM00409; IG; 3.
SMART; SM00406; IG; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKB; 3.
PROSITE; PS002209; IG MC; UNKNOWN 2.
SRQUENCE 479 AA; 52354 MW; 1692EF3457BE686E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
IGHG1 protein.
Name=IGHG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 AA.
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InterPro; IPR003596; Ig v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEPJA4 HUMAN PRELIMINARY;
QEPJA4;
                                                                                                                                                                                                                                                   Best Local Similarity 66.9
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
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TISSUE=Primary B-Cells;
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**X TABLES-LY-PROPAGE 12477932; DOI=10.1073/pnas.242603899;

**A KEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

**A KTAUSENE Z. Feingold R.A., Grouse L.H., Derge J.G.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Brownerein M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,

**A Robert S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

**Brownerein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

**A Raba S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Helton B.K. Ketteman M., Madan A., Young A.C., Shevichenko Y., Bouffard G.G.,

**Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

**A Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

**Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

**Butterfield N.S., Vonng A.C., Grimwood J., Schmutz J., Myers R.M.,

**Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

**Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYPYGTTYPDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 VDSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYMMSWVRQAPGKGLEWVANIKQDGSEKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 470;
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Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092518; AAH92518.1; -; mRNA.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF0764; Cl-et; 3.
SWART; SW00409; IG, 2.
SWART; SW00400; IGcl; 3.
SWART; SW00400; IGCl; 3.
PROSITE; PS000390; IG_MHC; UNKNOWN 2.
SRQUENCE 470 AA; 51716 MW; 7B49556A11PD7D99 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.0%; Score 435; DB 2;
70.2%; Pred. No. 9.5e-38;
iive 9; Mismatches 27;
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Matches 85; Conservative
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              PROSITE;
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TISSUE—Frimary B-Cells,

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSPERG R.L., Peringold B.A., Grouse L.H., Derge J.G.,

RIJURNET R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glubs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield R.M., Gorden E.D., Dickson M.A.,

Bodereation and initial analysis of more than 15,000 full-length human
                                                         3
                                                                                                                                         61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCA-RGIYFYGTTYFDYWGQGTLVTV 119
                                                                                                                                                          80 ADSVKGRPTISRDNSKNSLYLQMNSLRAEDTALYYCATRG--GYSTAGFDYWGQGTLVTV 137
                                                                                                   20 EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSLLSWDGGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                           Gaps
                                                        3,
                          66.9%; Score 434.5; DB 2; Length 469; 73.0%; Pred. No. 1.1e-37; ative 9; Mismatches 21; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041037; AAH41037.1; -; mRNA.
HNSP; POIGSG1, 1ADQ.
INTERPPO; IPRO01559; IG.
INTERPPO; IPRO01559; IG.
INTERPPO; IPRO03597; IG.
INTERPPO; IPRO03596; IG.
INTERPPO; IPRO03596; IG.
INTERPPO; IRRO03596; IG.
SMART; SMO0409; IG.; 2.
SMART; SMO0406; IG.; 3.
SMART; SMO0406; IG.; 1.
51254 MW; AC13448E3047784F CRC64;
                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                        89; Conservative
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NIH MGC Project;
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469 AA;
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                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          GHM protein.
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SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 VDSVKGRPTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYY--FYMDV 137
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Proteins 1:74-80(1986).
                                                                                                                                                                                                                                                                             1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                    20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMMSWVRQAPGKGLEWVANIKQDGSEKYY
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=79223895; PubMed=111245; Rao D.N., Rudikoff S., Krutzach H., Potter M.; Rad D.N., Rudikoff S., Krutzach H., Potter M.; Indikoff S., Krutzach H., Potter M.; Structural evidence for independent joining region gene in immoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-determining regions."; Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
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MEDLINE-88217852; PubMed=3449853; DOI=10.1002/prot.340010112;
Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A02080; AVMSJ5.
PDB; 2FBJ; X-ray; H=1-119.
SMR; P01810; 1-119.
SMR; P01810; 1-119.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM0406; IGv; 1.
3PR051TE; PS50835; Ig_LKE; 1.
3D-structure; Direct_protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                             12;
                                                                                                                                          Length 478;
                                                                                                                                                                                                         23; Indels
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG WHC; UNKNOWN 2.
SEQUENCE 478 AA; $\overline{5}2667 \text{ WW; 17BED38D917970D6 CRC64;}
                                                                                                                                      66.9%; Score 434; DB 2;
66.4%; Pred. No. 1.2e-37;
iive 9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV40 MOUSE STANDARD, PRT; 119 AA. P01810.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY PROTEIN SEQUENCE
                                                                                                                                                                                                         87; Conservative
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NON TER 119 119
STRAND 3 7
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85; Conservative
                                                                                                                                         QSULSO HUMAN PRELIMINARY;
QSULSO;
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                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                          117 VTVSS 121
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                                                                                                                                                                                                                                                          61 TPSLKDKPIISRDNAKNSLYLQMSKVRSEDTALYYCAR-LHYYG--YNAYWGGGTLVTVS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                          1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                    1 EVKLLESGGGLVQPGGSLKLSCAASGPDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                    66.8%; Score 433.5; DB 1; Length 119; 66.1%; Pred. No. 2.8e-38; ive 20; Mismatches 18; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 433; DB 2; Length 121; 69.6%; Pred. No. 3.2e-38; ive 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                   13240 MW; 577B4F1DB675C1F1 CRC64;
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EMBL; AR035043; AAD56279.1; -; mRNA.
HSSP; P01852; INPD.
SMR; OgUL71; 1-121.
Ensembl; ENSG0000130076; Homo sapiens.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IRR03596; Ig-v.
SWART; SM00406; IGV; I.
                                                                                                                                                                                                                                                                                                                                                     121 AA.
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Best Local Similarity 66.1%
Matches 80; Conservative
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Best Local Similarity 69.6%
Matches 87; Conservative
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                     121
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Homo sapiens (Human)
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                                                                                                                                          112 ;
119 AA;
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                                                                                                                                     61 NOKFKORFTISVDKSKNTLYLOMNSLRAEDTAVYYCARG----IYFYGTTYFDYWGQGTL 116
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Raaphorst F.M., Timmers B., Kenter M.J., Van Tol M.J., Vossen J.M., Schuurman R.K.;
Schuurman R.K.;
Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.";
EMBL; AP035024; AAD56260.1; -; mRNA.
EMBL; AP035024; AAD56260.1; -; mRNA.
HSSP; PO1772; 2FB4.
SNR; G9UL90; 1-113.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
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Mammalla, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
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PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                          Makiya R., Stigbrand T., "Placental alkaline phosphatase has a binding site for the human immunoglobuline G Pc portlon."; Bur. J. Blochem. 205:341-345(1992).
EMEL, J. PRO35023; AAD56259.1; -; mRNA.
                                                                                                                                                                                                               Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                              MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                               Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.0%; Score 428.5; DB 2; Length 118; 70.8%; Pred. No. 9.5e-38; Live 10; Mismatches 22; Indels 3
                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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118 AA; 12843 MW; D0633949F2AC149D CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
19 heavy chain V region X24.
Mus musculus (Mouse).
                     118 AA.
                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
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                     PRT;
                                          Created)
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InterPro; IPR003596; Ig v.
SMART; SM00406; IGv; 1.
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                                        01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                 QUL91 HUMAN PRELIMINARY;
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hes 85; Conservative
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PIR; S21205; S21205.
PIR; S30531; S30531.
HSSP; PO1783; IGC.
SMR; Q9UL91; 1-117.
                                                                                                 Homo sapiens (Human)
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUCLEOTIDE SEQUENCE OF 103-117.

MEDLINE=92355114; PubMed=1644448; DOI=10.1007/BF00215659;

Solin M.L., Kaartinen M.;

"Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy chain joining (JH) segments.";

Immunogenetics 36:306-313(1992).

-I MISCELLANEOUS: This chain was isolated from an IgA myeloma protein that binds galactan.

-I SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                         MEDLINE-79223895; PubMed=111245; Rao D.N., Rudikoff S., Krutzach H., Potter M.; Rudikoff S., Krutzach H., Potter M.; Structural evidence for independent joining region gene in immunoglobulin heavy chains from anti-galactan myeloma proteins and its potential role in generating diversity in complementarity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 118;
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HSSP, PO1810; 2FBJ.
SMR; PO1809; 1-118.
Ensembl; ENSMUSG0000003483; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003564; Ig-v.
PR051TB; PS080356; Ig L.
PR051TB; PS0835; IG LIKE; I.
Direct protein sequencing; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                        determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979)
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66.9%; Pred. No. 1.1e-37;
iive 17; Mismatches 19;
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                                                               Muroidea; Muridae; Murinae; Mus
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                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                 PROTEIN SEQUENCE.
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Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAM Way
CITY: SOUth San Francisco
STATE: California
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18 FORM:
COMPUTER: 18 FOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Peb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/974,899
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40.378
REFERENCE/DOCKET NUMBER: P1014R1
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SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-795-798-24
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ELEMPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-795-798-24
; Sequence 24, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
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425.257 Million cell updates/sec
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'cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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                                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-727-737-17
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US-10-815-641-20
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Minimum DB Maximum DB

Database

Result No.

Searched:

Sequence:

Run on:

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Indels

Length 121;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             Sequence 17, Application US/1072737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/975,329B
FLIING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPRENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear SEQID NO: 17: US-10-727-737-17
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 121 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
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RESULT 3

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                                                                           Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          Sequence 5, Application US/10727737;
Publication No. US20040146507A1
GENERAL INFORMATION:
TITLE OF INVENTION: Abribody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
STRRET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P1014R1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                      ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
Sequence 5, Application US/09795798
Publication No. US200310207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 121 amino acide TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                               1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                           Gaps
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Publication No. US20030021790A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Koumenis, Iphigenia
APPLICANT: Econg, Steven R.
APPLICANT: Prests, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
ITILE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-42-42-44
US Sequence 4, Application US/10423299
PUblication No. US2003022212A1
GENERAL INFORMATION:
APPLICANT: FARNER, ROBERT
APPLICANT: FOLIMAN, DEBORAH
APPLICANT: VAN REIS, ROBERT
TITLE OF INVENTION NON-APPLINITY PURIFICATION OF PROTEINS
FILE REFERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT PLILING DATE: 2003-04-25
PRIOR APPLICATION UNMBER: US 60/375,953
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
ILENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.4%; Score 632; DB 4; Length 451; Best Local Similarity 96.7%; Pred. No. 1.1e-49; Matches 117; Conservative 1; Mismatches 3; Indels
Best Local Similarity 96.7%; Pred. No. 2.8e-50; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Sequence is synthesized US-10-423-299-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
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US-09-726-258-50
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APPLICANT: LAVERDIERE, ANY
APPLICANT: LAVERDIERE, ANY
APPLICANT: LAVERDIERE, ANY
APPLICANT: MOUNALD, PAUL
APPLICANT: MOUNALD, PAUL
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRA
TITLE OF INVENTION: NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
CURRENT FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NOS: 8
TENCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQKFKDRFTISVDKSKNTLYLQMNSLRABDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKEKDRFTISVDKSKATILYLOMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.4%; Score 632; DB 4; Length 121; Best Local Similarity 96.7%; Pred. No. 2.8e-50; Matches 117; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.4%; Score 632; DB 5; Length 121;
                                                                      COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WAIRBAIN (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/727,737 FILING DATE: 03-Dec-2003 FILING DATE: 03-Dec-2003 FILING DATE: 03-Dec-2003 FILING DATE: 20-NOV-1997 APPLICATION NUMBER: US/08/975,329B FILING DATE: 27-NOV-1996 FILING DATE: 27-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lee, Wendy M.
REGISTRATION UNMER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-6
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 121 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10877532 Publication No. US20050038231A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                        ZIP: 94080
COMPUTER READABLE FORM:
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61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTT--YFDYWGQGTLVT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGYTMNWVRQAPGKGLEWVALINPYKGVSTY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Addrew Chan
APPLICANT: Qian Gong
APPLICANT: Olan Gong
APPLICANT: Olan Gong
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040R1US
CURRENT APPLICATION NUMBER: US/10/861,049
CURRENT PILING DATE: 2003-06-06
PRIOR PFLING DATE: 2003-06-06
PRIOR PFLING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-05
PRIOR PELLING DATE: 2003-06-05
PRIOR PELLING DATE: 2003-06-05
PRIOR PILING DATE: 2003-06-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
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Pred. No. 4.8e-40;
4; Mismatches 13
                                                                                                                                                                                                               REGISTRATION NUMBER: 40,378
REPERRICYS/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
APPLICATION NUMBER: US/09/705,398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: sequence is synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
                                                  APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
                                                                                                       APPLICATION NUMBER: 07/115272
FILING DATE: 14-7UN-1991
ATTORNATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 46, Application US/10861049; Publication No. US20050095243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 122 amino acide TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.7%;
Matches 103; Conservative
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ORGANISM: Artificial sequence
                              FILING DATE:
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US-10-861-049-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.5%; Score 548.5; DB 3; Length 116;
88.8%; Pred. No. 1.2e-42;
.ive 2; Mismatches 10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAARGIYFYGTTYFDYWGQGT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYC-ARGIYFYGTTYFDYWGQGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: G.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/726,258
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATE:
APPLICATION NUMBER: 09/234,182
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APPLICATION NUMBER: US/10/835,641
FILING DATE: 30-Apr-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/094003
PILING DATE: 24-UUL-1998
ATTONBY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650/252-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10835641
Publication No. US20040236078A1
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
South San Francisco
California
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Best Local Similarity 88.8<sup>3</sup>
Matches 103; Conservative
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TOPOLOGY: Linear
                                                                                                          94080
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                                                                           COUNTRY:
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1 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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; FEATURE:
; OTHER INFORMATION: humanized sequence
US-10-818-765-2
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US-10-922-651-2
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                      61 NQKFKGRPTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSASYWYFDVWGQGTLVTV 120
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TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
TITLE OF INVENTION: INADEQUATE RESPONSE TO A TNP-a INHIBITOR
TILE REPERBNES: P2027AL-US
CURRENT APPLICATION NUMBER: US/10/818,765
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: US 60/461,4819
PRIOR APPLICATION NUMBER: US 60/461,4819
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                        APPLICANT: Addrew Chan
APPLICANT: Qian Gong
APPLICANT: Qian Gong
APPLICANT: Plantew Chan
APPLICANT: Plantew Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040R1P1
CURRENT PAPLICATION NUMBER: US/11/021,874
CURRENT PILING DATE: 2004-06-04
FRIOR APPLICATION NUMBER: US 60/476,531
FRIOR APPLICATION NUMBER: US 60/476,531
FRIOR PILING DATE: 2003-06-05
FRIOR FILING DATE: 2003-06-05
FRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 46
IENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.7%; Score 517.5; DB 6; Length 452; Best Local Similarity 82.0%; Pred. No. 3.4e-39; Matches 100; Conservative 8; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: sequence is synthesized US-11-021-874-46
                                                                                                                                                                                              US-11-021-874-46
i. Sequence 46, Application US/11021874
i. Publication No. US20050163775A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10818765
Publication No. US20040202658A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial sequence
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                                                                                                                 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                                           Gaps
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; Sequence 2, Application US/10877363
; Publication No. US20050032130A1
; GENERAL INFORMATION:
    APPLICANT: BERESINI, MAUREEN
; APPLICANT: BONG, AN
    TITLE OF INVENTION INDIRER: US/10/877,363
; CURRENT APPLICATION UNMBER: US/10/877,363
; CURRENT FILING DATE: 2004-24
; PRIOR PPLICATION NUMBER: US 60/490,678
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
                                                           1;
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  Length 122;
79.6%; Score 516.5; DB 4; Length 82.0%; Pred. No. 1.1e-39; ive 7; Mismatches 14; Indels
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82.0%; Pred. No. 1.1e-39;
tive 7; Mismatches 14;
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) Publication No. US20050053602A1
) GENERAL INFORMATION:
) APPLICANT: BRUMETTA, PAUL G.

TITLE OF INVENTION: Therapy of Ocular Disorders
PILE REPRENCE: P2029R1
) CURRENT APPLICATION NUMBER: US/10/922,651
CURRENT FILING DATE: 2004-08-20
) PRIOR APPLICATION NUMBER: US 60/498,791
) PRIOR PILING DATE: 2003-08-29
) NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Sequence is synthesized. US-10-877-363-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial sequence
  Query Match 79.6
Best Local Similarity 82.0
Matches 100; Conservative
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Best Local Similarity 82.0
Matches 100; Conservative
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| Sequence 14, Application US/10861049
| Publication No. US20S0095243A1
| Publication No. US20S0095243A1
| GENERAL INFORMATION:
| APPLICANT: Andrew Chan
| APPLICANT: Andrew Chan
| APPLICANT: Plavius Martin
| TILE OF INVENITON: COMBINATION THERAPY FOR B CELL DISORDERS
| TILE REPRENCE: P2040R103
| CURRENT APPLICATION NUMBER: US/10/861,049
| CURRENT APPLICATION NUMBER: US 60/476,531
| PRIOR PLING DATE: 2003-06-06
| PRIOR PLING DATE: 2003-06-05
| PRIOR PLING DATE: 2003-06-05
| PRIOR RILING DATE: 2003-06-05
| PRIOR RILING DATE: 2003-06-05
| PRIOR RILING DATE: 2003-06-05
| NUMBER OF SEQ ID NOS: 145
| LENGTH: 122
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                                                                                                                                                                                                   DB 5; Length 122;
                                                                                                                                                                                            Query Match 79.6%; Score 516.5; DB 5; Length Best Local Similarity 82.0%; Pred. No. 1.1e-39; Matches 100; Conservative 7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.6%; Score 516.5; DB 5; Length Best Local Similarity 82.0%; Pred. No. 1.1e-39; Matches 100; Conservative 7; Mismatches 14; Indels
                                         TYPE: PRT
ORGANISM: Artificial sequence
FRATURE:
OTHER INFORMATION: Sequence is synthesized.
US-10-922-651-2
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US-11-021-874-14
US-11-021-874-14
; Paquence 14, Application US/11021874
; Publication No. US20050163775A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
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SEQ ID NO 2
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| APPLICANT: Andrew Chan
| APPLICANT: Andrew Chan
| APPLICANT: Andrew Chan
| APPLICANT: Andrew Chan
| APPLICANT: Plavius Martin
| TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
| TITLE OF INVENTION WINDER: US/11/021,874
| CURRENT FILING DATE: 2004-06-04
| FRIOR FILING DATE: 2004-06-04
| FRIOR PLING DATE: 2003-06-05
| FRIOR PL
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NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEPHONE: 650/225-4461

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID US-10-665-658-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 121 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
\begin{array}{c} \mathbf{c} & \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-665-658-24
April 13, 2006, 17:21:05; Search time 17:9651 Seconds (without alignments) 286.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 5, 1
                                                                                                                                                                                                                                                                                                                   US-10-727-737-17
649
1 BVQLVBSGGGLVQPGGSLRL.......FYGTTYFDXWGQGTLVTVSS 121
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1: /SIDS5/ptcdata/1/pubpaa/US08 NEW PUB.pep:*
2: /SIDS5/ptcdata/1/pubpaa/US06 NEW PUB.pep:*
3: /SIDS5/ptcdata/1/pubpaa/US07 NEW PUB.pep:*
4: /SIDS5/ptcdata/1/pubpaa/PCT_NEW PUB.pep:*
5: /SIDS5/ptcdata/1/pubpaa/US10_NEW PUB.pep:*
6: /SIDS5/ptcdata/1/pubpaa/US10_NEW PUB.pep:*
7: /SIDS5/ptcdata/1/pubpaa/US11 NEW PUB.pep:*
8: /SIDS5/ptcdata/1/pubpaa/US11 NEW PUB.pep:*
                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-167-0028-50

US-11-149-0011-2

US-11-120-318-24

US-11-120-318-24

US-11-120-318-24

US-11-120-32-45

US-11-120-32-45

US-11-120-338-17-22

US-11-120-338-17-22

US-11-120-338-17-22

US-11-143-38-25

US-11-107-028-47

US-11-106-920-45

US-11-106-920-45

US-11-107-028-47

US-11-106-920-45

US-11-107-028-47

US-11-107-028-47

US-11-107-028-47
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US-11-107-028-46
US-11-106-820-30
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match 1
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Perfect score:
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Maximum DB 8
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TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
ADDRESSE Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IRM PC COMPAthle OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
US-11-208-422-40

US-11-208-422-43

US-11-208-32-44

US-11-120-338-8

US-11-107-028-30

US-11-143-077-8

US-11-143-36-8

US-11-143-386-8

US-11-143-386-8

US-11-143-386-8

US-11-120-338-22

US-11-120-338-14

US-11-120-338-14

US-11-120-338-14

US-11-120-338-14

US-11-120-338-14

US-11-120-338-14

US-11-107-028-32

US-11-107-028-33

US-11-106-820-28
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APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-56p-2003
CLASSIFICATION AUTHER: US/10/665,658
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/91899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/975798
FILING DATE: 20-CT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 20-CT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
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Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
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NO: 24:

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                                                                                                            1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMWWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                1 BVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
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                                           Gaps
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  DB 6; Length 121;
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                                         0; Indels
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Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.4%; Score 632; DB 6; Best Local Similarity 96.7%; Pred. No. 7.3e-45; Matches 117; Conservative 1; Mismatches 3
100.0%; Score 649; DB 6
100.0%; Pred. No. 3e-46;
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: Callfornia
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/1065558
Publication No. US20050276801A1
GENERAL INFORMATION:
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
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TYPE: Amino Acid
                 Best Local Similarity 100.
Matches 121; Conservative
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DB 7; Length 122;

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61 NQKFKGRPTISVDKSKONTLYLQMNSLRAEDTAVYYCARVVYYSSYRYWYFDVWGQGTLVTV 120
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                                                                                                                                                                                                                                                                                        1 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                       Query Match 80.4%; Score 521.5; DB 7; Best Local Similarity 82.8%; Pred. No. 6.8e-36; Matches 101; Conservative 7; Mismatches 13;
                                                                                                                                         ; OTHER INFORMATION: sequence is synthesized US-11-120-338-24
                                                                                TYPE: PRT
ORGANISM: Artificial sequence
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 24
LENGTH: 122
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Best Local Similarity
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APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Marvin, POLYBEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE REFERENCE: P2158R1
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT APPLICATION NUMBER: US/11/208,422
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
                                                                                                     1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIAPASSSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
                                                                                                                                            EVOLVESGGGLVQPGGSLRLSCAASGYSPTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY
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                                                             Gaps
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                Score 632; DB 7; Length 121;
Pred. No. 7.3e-45;
1; Mismatches 3; Indels
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Sequence 24, Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
APPLICANT: WALLCKE, PATRICIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 632; DB 7;
Pred. No. 7.3e-45;
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96.7%; Pred. No. /...
'... 1; Mismatches
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US-11-208-422-14
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 14, Application US/11208422; Publication No. US20060067930A1; GENERAL INFORMATION:
                   97.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.7<sup>3</sup>
Matches 117; Conservative
                     Query Match
Best Local Similarity 96.7
Matches 117; Conservative
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SEQ ID NO 14
LENGTH: 121
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61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVYYCARGIYF-YGTTYFDYWGQGTLVTV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7;
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                                                                                                                  APPLICANT: Brunetta, Paul G.
TITLE OF INVENTION: METHOD FOR TREATING LUPUS
FILE REFERENCE: P2133R1
CURRENT APPLICATION NUMBER: US/11/143,077
CURRENT FILING DATE: 2005-06-02
FRIOR APPLICATION NUMBER: US 60/577,235
FRIOR PILING DATE: 2004-06-04
FRIOR PILING DATE: 2004-06-04
FRIOR PILING DATE: 2004-06-04
FRIOR FILING DATE: 2004-10-11
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Sequence 24. Application US/11143386
Publication No. US20060051345A1
GENERAL INFORMATION:
APPLICANT: FROHNA, PAUL A.
US-11-143-077-24
; Sequence 24, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial sequence
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CURRENT APPLICATION NUMBER: US/11/120,338 CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: US 60/568,460

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61 NQKFKGRFTISVDKSKONTLYLQMNSLRAEDTAVYYYGARVVYYSYRYWYFDVWGQGTLVTV 120
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                                                APPLICANT: Adams, Camellia W. APPLICANT: Adams, Camellia W. APPLICANT: Lien, Samantha APPLICANT: Lien, Samantha APPLICANT: Lowman, Henry B. APPLICANT: Meng, Yu-Ju G. TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION CURRENT APPLICATION NUMBER: US/11/208,422 CURRENT FILING DATE: 2005-08-19 PRIOR APPLICATION NUMBER: US 60/603,057 PRIOR PILING DATE: 2004-08-19 NUMBER OF SEQ ID NOS: 54
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Pred. No. 6.8e-36;
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| Sequence 25, Application US/11120338
| Publication No. US20050271658A1
| GENERAL INFORMATION:
| APPLICANT: BRUNETTA, PAUL G.
| APPLICANT: GREWAL, IQBAL S.
| TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE;
| TILLE REFERENCE: P2079R2
| CURRENT PPLICATION NUMBER: US/11/120,338
| CURRENT PPLICATION NUMBER: US 60/568,460
| PRIOR APPLICATION DATE: 2005-05-03
| NUMBER OF SEQ ID NOS: 25
| NUMBER OF SEQ ID NOS: 25
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80.4%; Score 521.5; D
Best Local Similarity 82.8%; Pred. No. 6.8e-
Matches 101; Conservative 7; Mismatches
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ORGANISM: Artificial sequence
            No. US20060067930A1
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                                          GENERAL INFORMATION
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TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS FILE REFERENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/576,993
PRIOR PILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.4%; Score 521.5; DB 7; Length Best Local Similarity 82.8%; Pred. No. 6.8e-36; Matches 101; Conservative 7; Mismatches 13; Indels
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TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME
FILE REFERENCE: P2149R1
CURRENT APPLICATION NUMBER: US/11/187,364
CURRENT APPLICATION NUMBER: US/0/590,302
PRIOR APPLICATION NUMBER: US 60/590,302
PRIOR FILING DATE: 2004-07-22
PRIOR FILING DATE: 2004-07-22
SRQ ID NO 36
LENGTH: 122
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5-11-208-422-45
Sequence 45, Application US/11208422
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; Sequence 36, Application US/11187364
; Publication No. US20060062787A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial sequence
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61 NQKFKGRFTISVDKSKONTLYLQMNSLRAEDTAVYYCARVVYYSYRYWYFDVWGQGTLVTV 120
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1 EVQLVESGGGLVQPGGSLRLSCAASGYTPTSYNMHWVRQAPGKGLEWVGAIYPGNGATSY 60
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hitraya, Blena
TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROWE
FILE REFERENCE: P2149F1
CURRENT APPLICATION NUMBER: US/11/187,364
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/590,302
PRIOR PILING DATE: 2004-07-22
NUMBER OF SEQ ID NOS: 36
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Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
APPLICANT: GREWAL, IQBAL S.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR PILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 17
LENGTH: 452
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; OTHER INFORMATION: Sequence is synthesized
US-11-187-364-34
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Publication No. US20060062787A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Best Local Similarity 82.8°
Matches 101, Conservative
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US-11-120-338-17
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LENGTH: 45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 451;
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Sequence 25, Application US/11143386
Sequence 25, Application US/11143386
Sequence 25, Application US/11143386
Sequence 25, Application US/11143386
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS FILE REPERMICE: P2134R1
CURRENT PILITG DATE: 2005-06-02
PRIOR PILING DATE: 2005-06-04
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 25
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 521.5; DB 7; Length Pred. No. 2e-35; 7; Mismatches 13; Indels
                                                                                                                                                                      Sequence 22, Application US/11143077
Publication No. US20060024295A1
GENERAL INFORMATION:
APPLICANT: Brunetta, Paul G.
TITLE OP INVENTION: METHOD FOR TREATING LUPUS:
FILE REPRENCE: P2133R1
CURRENT APPLICATION NUMBER: US/11/143,077
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/577,235
PRIOR APPLICATION NUMBER: US 60/617,997
PRIOR PILING DATE: 2004-06-04
PRIOR PILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 22
LENGTH: 451
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, OTHER INFORMATION: Sequence is synthesized
US-11-143-077-22
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82.8%;
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Best Local Similarity
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Best Local Similarity 82.8%; Pred. No. 2e-35;
Matches 101; Conservative 7; Mismatches 13; Indels
                                                                                                                     Search completed: April 13, 2006, 17:25:17 Job time : 17.9651 seca
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                      8 6 6 6 6
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Sequence Sequence Sequence Sequence

US-11-051-453-46 US-11-127-932-14 US-11-127-933-18 US-11-127-903-18 US-11-127-903-18 US-11-127-903-18 US-11-199-739-700 US-11-199-739-700 US-11-199-739-700 US-11-199-739-700 US-11-109-739-739-739-739 US-11-041-095-13 US-11-041-095-13 US-11-102-512-3 US-11-102-512-3

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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US-10-665-658-2

Sequence 2, Application US/10665658

Sequence 2, Application US/10665688

Publication No. US20050276801A1

GENERAL INFORMATION:

Presta, Leonard G.

TILE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: COUNTRY: USA

ZIP: 94080

COMPUTER: READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) APPLICATION DATA: APPLICATION NUMBER: US/10/665,658 FILING DATE: 19-Sep-2003 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650/225-4462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Tan, Lee K.
                                       April 13, 2006, 17:21:05 ; Search time 16.0349 Seconds (without alignments) 286.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 49,
Sequence 1,
Sequence 3,
                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVT......QQHNEYPLTFGQGTKVEIKR 108
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1: /SIDSS/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

2: /SIDSS/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

3: /SIDSS/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

4: /SIDSS/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /SIDSS/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

7: /SIDSS/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

8: /SIDSS/ptcdata/1/pubpaa/US11_NEW_PUB.pep:*
                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-096-046-5
US-11-154-337-5
US-11-182-908-5
US-11-102-120-5
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US-11-127-677-75
US-11-051-453-32
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length D
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Perfect score:
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1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
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Best Local Similarity 100.0%; Pred. No. 5.9e-39;
Matches 108; Conservative 0; Mismatches 0;
                     ) OTHER INFORMATION: Sequence is synthesized US-11-208-422-15
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US-11-107-028-49
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FEATURE:
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APPLICANT: Lien, Samantha
APPLICANT: Lownan, Henry B.
APPLICANT: Lownan, Henry B.
APPLICANT: Meng, Yu-Ju G.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REFERENCE: P2158R1
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR PLING DATE: 2004-08-19
SEQ ID NOS: 54
SEQ ID NOS: 54
TYPE: PRT
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                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
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APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Mary Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE REFERENCE: P2158R1
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                                                                                                                                                                                                                                                                               61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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                  Query Match 100.0%; Score 560; DB 6; Length 108; Best Local Similarity 100.0%; Pred. No. 3.2e-39; Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 560; DB 7; Length 108; Best Local Similarity 100.0%; Pred. No. 3.2e-39; Matches 108; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
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Publication No. US20060067930A1
GENERAL INFORMATION:
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US-11-208-422-15
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1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
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TITLE OF INVENTION: Method of Treating Granuloma Annulare or Sarcoid
FILE REFERENCE: P2129R1
CURRENT APPLICATION NUMBER: US/11/149,031
CURRENT FILING DATE: 2005-06-08
PRIOR FILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-06-09
RIOR FILING DATE: 2004-06-10
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                                                                                                                          61 RFSGSGSGTDFTLTISSLOPEDPATYYCQQHNEYPLTFGGGTKVEIKR 108
                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CHAN, ANDREW C.
APPLICANT: GONG, QIAN
APPLICANT: GONG, QIAN
APPLICANT: MARTIN, FLAVIUS
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REPERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT FILING DATE: 2005-04-15
PRIOR PILING DATE: 2004-04-16
SEQ ID NO 49
LENGTH: 107
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Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: sequence is synthesized
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; Publication No. US20050276803A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/11149031; Publication No. US20060013818A1; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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97; Conservative
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Best Local (
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                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
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                                                                                                                0; Gaps
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90.4%; Score 506; DB 6; Length 108;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5; Indels
                                                                Length 107;
                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
FILING DATE: 27-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/420745
FILING DATE: 28-FEB-2001
ATTORNEY/AGRY INCORMATION:
                                                                Query Match 99.1%; Score 555; DB 7; I
Best Local Similarity 100.0%; Pred. No. 8.1e-39;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
; OTHER INFORMATION: sequence is synthesized US-11-149-031-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10665658 Publication No. US20050276801A1 GENERAL INFORMATION:
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYPE: Amino Acid
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US-10-665-658-3
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61 RFSGSGSGTDFTLTISSLQPEDPATYYCQQYNSLPWTFGQGTKVEIKR 108
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                                                                                                                                                               Sequence 3, Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION UNMER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US/11/120,338
PRIOR APPLICATION NUMBER: US/11/120,338
PRIOR APPLICATION NUMBER: US/11/120,338
SEQ ID NOS: 25
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Pred. No. 7.9e-35;
6; Mismatches 5;
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Fublication No. US2066024295A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: METHOD FOR TREATING LUPUS
FILE REFERENCE: P2133R1
CURRENT APPLICATION NUMBER: US/11/143,077
CURRENT FILING DATE: 2005-06-02
FRIOR APPLICATION NUMBER: US 60/577,235
FRIOR APPLICATION NUMBER: US 60/577,235
FRIOR APPLICATION NUMBER: US 60/617,997
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Pred. No. 7.9e-35;
6; Mismatches 5
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ORGANISM: Artificial Sequence
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Best Local Similarity 89.8%;
Matches 97; Conservative
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1 DIOMIQSPSSLSASVGDRVITTCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
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     1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
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                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
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                                                                                                                                                                                                                                                                                       Sequence 3, Application US/11143386;
Publication No. US20060051345A1;
GENERAL INFORMATION:
APPLICANT: FROHMA, PAUL A.
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
FILE REFERENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2004-06-02;
PRIOR APPLICATION NUMBER: US 60/576,993
FRIOR FILING DATE: 2004-06-04;
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 3
LENGTH: 108
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Publication No. US20060062787A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR TREATING SJOGREN'S SYNDROME;
FILE REFERENCE: P2149R1;
CURRENT APPLICATION NUMBER: US/11/187,364;
CURRENT FILING DATE: 2005-07-21;
PRIOR APPLICATION NUMBER: US 60/590,302;
NUMBER OF SEQ ID NOS: 36;
SEQ ID NO 3
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Pred. No. 7.9e-35;
6; Mismatches 5; Indels
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; OTHER INFORMATION: Sequence is synthesized.
US-11-143-386-3
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l Similarity 89.8%;
97; Conservative 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-187-364-3
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Best Local Similarity
Matches 97; Conservat
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                                                                                                    RESULT 9
US-11-190-364-3
i Sequence 3, Application US/11190364
i Publication No. US20060024300A1
i GENERAL INPORMATION:
I TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
FILE REPERENCE: P1990R3C1P1
i CURRENT PILING DATE: 2005-07-26
FRIOR APPLICATION NUMBER: US 60/434,115
i PRIOR PILING DATE: 2002-12-16
i PRIOR APPLICATION NUMBER: US 60/526,163
i PRIOR FILING DATE: 2003-12-01
i PRIOR FILING DATE: 2003-12-16
i PRIOR PILING DATE: 2005-06-07
i NUMBER OF SEQ ID NOS: 38
i EBNOTH: 108
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Fublication No. US20060034835A1
Fublication No. US20060034835A1
GENERAL INFORMATION:
APPLICANT: Adams ET AL.
TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
FILE REPRENCE:
CURRENT APPLICATION NUMBER: US/11/147,780
CURRENT APPLICATION NUMBER: US 60/434,115
PRIOR PPLICATION NUMBER: US 60/434,115
PRIOR PPLICATION NUMBER: US 60/526,163
PRIOR APPLICATION NUMBER: US 60/526,163
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR APPLICATION NUMBER: PCT/US03/40426
PRIOR PILING DATE: 2003-12-01
PRIOR PILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 38
LENGTH: 108
RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIKR 108
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90.4%; Score 506; DB 7;
Best Local Similarity 89.8%; Pred. No. 7.9e-35;
Matches 97; Conservative 6; Mismatches 5;
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; OTHER INFORMATION: Sequence is synthesized
US-11-147-780-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Sequence is synthesized
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Search completed: April 13, 2006, 17:25:18 Job time: 17.0349 secs
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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                                                                     Sequence 5, Application US/10981356A
Fublication No. US20060015952A1
Fublication No. US20060015952A1
Fublication No. US20060015952A1
Fublication No. US20060015952A1
Fublication No. US2006001595A1
Fublication Number SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
FULL REPRENENCE: 2004-11-04
FUCRENT PILING DATE: 2004-11-04
FRIOR PILING DATE: 2004-11-04
FRIOR PLICATION NUMBER: US 60/520,398
FRIOR PLICATION NUMBER: US 60/520,398
FRIOR APPLICATION NUMBER: US 60/557,951
FRIOR PLICATION NUMBER: US 60/557,951
FRIOR FILING DATE: 2004-03-31
FRIOR FILING DATE: 2004-03-31
FRIOR FULL REATMENT NUMBER: US 60/557,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.4%; Score 506; DB 6; Length 109; Best Local Similarity 89.8%; Pred. No. 8e-35; Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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Publication No. US20050276802A1

GENERAL INPORMATION:
APPLICANT: ADAMS, CAMELLIA W.
APPLICANT: PERRARA, NAPOLEONE
APPLICANT: PRIVAROFF, BLIEN H.
APPLICANT: PRISTANG
APPLICANT: PRISTANG
APPLICANT: PRISTAN LEGONAR
APPLICANT: PRISTA, LEGONAR
APPLICANT: PRISTA, LEGONAR
FILE REFERENCE: PISJAFRIUS
CURRENT APPLICANTON: Humanized Anti-TGP-Beta Antibodies
FILE REFERENCE: PISJAFRIUS
CURRENT APPLICANTON NUMBER: US/11/096,046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.4%; Score 506; DB 7;
89.8%; Pred. No. 8e-35;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Sequence is synthesized U3-10-981-356A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
PEATURE:
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Best Local Similarity 89.8
Matches 97; Conservative
                                                         US-10-981-356A-5
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61 RPSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108

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1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
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61 RFSGSGSGTDPTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 501; DB 7; Length 107;
Pred. No. 2e-34;
6; Mismatches 5; Indels
                                                                                                                                                          Sequence 5, Application US/11154337
Publication No. US20060013819A1
GENERAL INPORMATION:
I TITLE OF INVENTION: THERAPY OF PLATINUM-RESISTANT CANCER
FILE REPREMENCE: P2146R1
CURRENT APPLICATION NUMBER: US/11/154,337
CURRENT FILING DATE: 2005-06-15
PRIOR FILLING DATE: 2004-06-16
NUMBER: OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: sequence is synthesized US-11-154-337-5
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Title: Perfect score:

Run on:

Sequence

Scoring table:

Searched:

Database

Result

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1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDER: 24
CORRESPONDER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-10-125-687-8

US-10-996-191-8

US-10-725-962-36

US-10-725-962-36

US-10-800-533-30

US-10-800-533-30

US-10-625-105-30

US-10-625-105-30

US-10-469-125-8

US-10-910-910-20

US-10-910-910-44

US-10-910-910-44

US-10-910-910-44

US-10-923-191-6

US-10-923-191-6

US-10-923-191-6

US-10-292-088-105

US-10-292-088-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: «Unknown»
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Windatin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28 Feb-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                  ALIGNMENTS
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09795798 Publication No. US20030207336A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 108; Conservative
    US-09-795-798-2
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    RESULT 1
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                                                                                           April 13, 2006, 17:19:49; Search time 106.114 Seconds (without alignments) 425.257 Million cell updates/sec
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Sequence 3, 1
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Sequence 5
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Sequence
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-811-123-6
US-10-044-896-4
US-09-809-739-10
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US-09-795-798-3
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US-10-974-591-12
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US-10-835-641-3
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                                                                                                                                                                                                                                        1867569 seqs, 417829326 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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560
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Match Length
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US-09-726-258-47
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RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                            61 RFSGSGGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPAtin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/10/727,737

FILING DATE: 03-Dec-2003

CLASSIFICATION: «Unknown»

PRIOR APPLICATION NUMBER: US/08/975,329B

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 60/031945

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10877532
PUBLICATION NO. US20050038231A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT L.
APPLICANT: APPLICANT:
APPLICANT: MCDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.
                                                                                                                                                        Sequence 2, Application US/10727737 Publication No. US20040146507A1 GENERAL INFORMATION:
                                                                                                                                    US-10-727-737-2
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TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAFIER REPREBRICE: P2015R1
CURRENT APPLICATION NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: US 60/490,500
PRIOR APPLICATION NUMBER: US 60/490,500
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVBIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 560; DB 5; Length 108; Best Local Similarity 100.0%; Pred. No. 4e-39; Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR
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BUDICATION NO. US20030229212A1

GENERAL INFORMATION:
APPLICANT: PAHRNER, ROBERT
APPLICANT: FOLLMAN, DEBORAH
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: UAN REIS, ROBERT
ITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
ITLE REPERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT APPLICATION NUMBER: 2003-04-25
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100.0%; Score 560; DB 4;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: sequence is synthesized

    FEATURE:
    OTHER INFORMATION: Sequence is synthesized
US-10-423-299-3

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PRIOR FILING DATE: 2002-04-26
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
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SEQ ID NO 3
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Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIOMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Sabara, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
CORRESPONDENCE ADDESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 SRPSGSGSGTDFTLTISSLOPEDPATYYCQQHNEYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.6%; Score 546.5; DB 3; Length 109; Best Local Similarity 98.2%; Pred. No. 5.4e-38; Matches 107; Conservative 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/726,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09056160B
Fatent No. US20020032315A1
GENERAL INFORMATION:
BAPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: Conth San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
APPLICATION NUMBER: 60/094003
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REPERENCE/DOCKET NUMBER: 91095R4-1A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-984.
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                        ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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COMPUTER: IN THE COMPANIES FORM:
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COMPUTER: IN THE COMPANIES FORM:
MEDITEM FIRST. 13 INC. 1.4 ND floppy disk
COMPUTER: IN THE COMPANIES FORM:
MEDITEM FIRST. 13 INC. 1.4 ND floppy disk
COMPUTER: IN THE COMPANIES FORM:
MEDITEM FIRST. 10 INC. 1.4 ND floppy disk
CLASSITICATION NATA:
MEDITEM ORDER: 60/104/1857
PRILICATION NATA:
MEDITEM ORDER: 60/104/1857
PRILICATION NATA:
MEDITEM ORDER: 60/104/1857
PRESENCE COMPUTER: 10 INC. 1.2 IN
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RESULT 10
US-10-861-049-38
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                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                   Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPATIN (Genentech)
                                                                                                                                                                                       Score 506; DB 3;
Pred. No. 1.2e-34;
6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear SEQ ID NO: 12: US-10-234-671-12
                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPE: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 108 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650/952-9881
MATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       ch
1 Similarity 89.8%;
97; Conservative
                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                 1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
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                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
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                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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Score 506; DB 4; Length 108;
Pred. No. 1.2e-34;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 13M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERRUE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Preets, Leonard G.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genentech, Inc.
STREEF: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 89.8%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 89.8
Matches 97; Conservative
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REGISTRATION NUMBER: 44,637
                               REFERENCE/DOCKET NUMBER: P
TELECOMUNICATION INPORMATION:
TELEPHONE: 650/225-8674
TELEPAX: 650/952-981
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-021-874-38
; Sequence 38, Application US/11021874
; Publication No. US20050163775A1
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Sequence 6, Application US/09811123
Patent No. US2002001587A1
GENERAL INFORMATION:
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Best Local Similarity 89.8%;
Matches 97; Conservative
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Best Local Similarity 89.8%;
Matches 97; Conservative
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ORGANISM: Homo sapiens
US-11-021-874-38
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                                              # PRUBLICATION NO. US20050095243A1

# PUBLICATION NO. US20050095243A1

# PRUBLICANT: ADDIEW Chan

# APPLICANT: Qian Gong

# APPLICANT: Qian Gong

# TITLE OF INVENTION: CCMBINATION THERAPY FOR B CELL DISORDERS

# TITLE OF INVENTION: CCMBINATION THERAPY FOR B CELL DISORDERS

# TITLE OF INVENTION: CCMBINATION THERAPY FOR B CELL DISORDERS

# TITLE OF INVENTION: CCMBINATION THERAPY

# PRIOR APPLICATION NUMBER: US 60/476,531

# PRIOR PILING DATE: 2003-06-06

# PRIOR PILING DATE: 2003-06-05

# PRIOR PILING DATE: 2003-06-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.4%; Score 506; DB 5; Length 108; 89.8%; Pred. No. 1.2e-34; tive 6; Mismatches 5; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
CLASSIPTCATION AURACHOMBA
PRICATICATION NUMBER: 09/723752
FILING DATE: 27-NOW-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/813504
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Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Callfornia
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Publication No. US20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
      Application US/10861049
No. US20050095243A1
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Best Local Similarity 89.8°
Matches 97; Conservative
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APPLICANT: Qian Gong
APPLICANT: Qian Gong
APPLICANT: Plantus Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REPERERRENCE: P2040R1P1
CURRENT APPLICATION NUMBER: US/11/021,874
CURRENT FILING DATE: 2004-12-22
PRIOR FILING DATE: 2004-06-04
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-06
PRIOR FILING DATE: 2003-06-05
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                                                                                                          Length 108;
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Pred. No. 1.2e-34;
6; Mismatches 5;
                                                                                                  Score 506; DB 5;
Pred. No. 1.2e-34;
6; Mismatches 5;
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 109;
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Pred. No. 1.3e-34;
6; Mismatches 5; Indels
                 TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-EAB
TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
FILE REFERENCE: GENERAT. 0.73.2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.4%; Score 506; DB 3; Length 10: Best Local Similarity 89.8%; Pred. No. 1.2e-34; Matches 97; Conservative 6; Mismatches 5; Indels
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Publication No. US20030166228A1

GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Stewart, Timothy
APPLICANT: Desta Leonard G
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENENT: 074A
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/27075
PRIOR PPLING DATE: 2001-02-22
NUMBER: FRESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6
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US-09-809-739-10
; Sequence 10, Application US/09809739
; Petent No. US20020106369A1
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89.8%;
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 89.84
Matches 97; Conservative
Mark Sliwkowski
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Search completed: April 13, 2006, 17:24:38 Job time : 107.114 secs

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FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Simi
Matches 108;
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Query Match
Best Local (
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Sequence 47, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 3, Appli
Sequence 18, Appli
                                                                                April 13, 2006, 17:19:00 ; Search time 31.5983 Seconds (without alignments) 282.578 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVT.....QQHNBYPLTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                1: /cgn2_6/ptodata/1/laa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/RB_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/RB_COMB.pep:*
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US-09-795-798-2
US-08-802-449-47
US-09-802-985-47
US-09-121-952A-47
US-09-355-014-47
US-09-355-014-47
US-08-908-469-3
US-08-908-469-3
US-08-908-469-3
US-09-105-798-3
US-09-105-798-3
US-09-105-398-3
US-08-37-642B-18
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US-09-705-686-18
US-09-705-392A-18
US-09-705-398-18
US-09-602-812A-5
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                US-10-727-737-2
560
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Match Length
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                                                                                                                                                                                                                                                                                                                                                           43,
                                                      Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
DCT-US93-07832-18
US-09-025-769B-28
US-09-025-769B-43
US-09-490-070A-28
US-09-490-153-28
US-09-490-153-28
US-09-490-153-43
US-09-490-324-28
US-09-490-324-28
US-09-490-324-3
US-09-490-324-3
US-09-490-324-3
US-09-65-769B-14
US-09-65-769B-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-920-262A-8
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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-192-854-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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REGISTRATION NUMBER: 40,378
REGISTRAFORCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-974-899-2; Sequence 2, Application US/08974899; Patent No. 6037454; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60/031971
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ADDRESSEE:
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APPLICANT: Leong, Steven R.
APPLICANT: Leong, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
CORRESPONDENCE ADDRESS:
                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 108
61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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100.0%; Score 560; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 108; Conservative 0; Mismatches 0; Indels
                                                                                                                                                             Sequence 2, Application US/09795798

Patent No. 6703018

GRNERAL INFORMATION:

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRNY APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-027-449-47; Sequence 47, Application US/09027449; Patent No. 6025158; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 108 amino acide
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                     RESULT 2
US-09-795-798-2
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1 DIQMIQSPSSLSASVGDRVIITCRASKIISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
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Sequence 47, Application US/08804444A

Patent No. 6117980

GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania N

APPLICANT: Leong, Steven R.

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

TITLE OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Prancisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 546.5; DB 2; Length Pred. No. 1.1e-40; 1; Mismatches 0; Indels
                                                                                                 ZUUNITER READABLE FORM:

MEDION TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION ATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 22-Jan-1998
RIGHER APPLICATION NUMBER: 60/038,64
FILING DATE: 22-Jan-1998
RIGHER APPLICATION NUMBER: 40/038,64
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 91085R3-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESTANTON:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Peb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                 South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 109 amino acids
Amino Acid
DNA Way
                                                                                      USA
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US-08-804-444A-47
                                                       STATE: C
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US-09-121-952A-47

US-09-121-952A-47

US-09-121-952A-47

Sequence 47, Application US/09121952A

Patent No. 645835

GENERAL INPORMATION:

APPLICANT: Roumenis, Iphigenia
APPLICANT: Roumenis, Iphigenia
APPLICANT: Bhahrokh, Zahra

APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra

APPLICANT: Shahrokh, Zahra

APPLICANT: WHITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES

NUMBER OF SEQUENCES;

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: I DNA Wav
1 DIOMIGSPSSLSASVGDRVIIICRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIXYSGSTLESGVP 60
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                                                                                                                                                                              61 SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/07430
FILING DATE: 22-JAN-1998
PRIOR APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFHONE: 650/25-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 109 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.6
Best Local Similarity 98.2
Matches 107; Conservative
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US-09-121-952A-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sequence 47, Application US/09026985

Patent No. 6131346

GENERAL INFORMATION:

APPLICANT: Leong, Steven R.

APPLICANT: Leong, Steven R.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSE: Genentech, Inc.

STREET: DNA Way

CITY: South Saw Francisco

STATE: California

CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.6%; Score 546.5; DB 2; Length 109; Best Local Similarity 98.2%; Pred. No. 1.1e-40; Matches 107; Conservative 1; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.6%; Score 546.5; DB 2; Length 109; 98.2%; Pred. No. 1.1e-40; tive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZOUNTINE STADDABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/026,985 FILING DATE: 20-Feb-1998 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: LOVE, RICHARD B. REGISTRATION NUMBER: 91085R3-1 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION 
                     ATTORNEY/AGENT INPORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/225-5530
TELEFAX: 650/252-9881
INFORMATION FOR SEQ ID NO: 47:
SEGUENCE TRARACTER.FSTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 47:
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Amino Acid
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Best Local Similarity 98.2
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
US-08-804-444A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear
   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-026-985-47
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RESULT 7

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1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLBSGVP 60
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                               Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genencech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-Jul-1999
CLASSIFICATION: <UNKNOWID>
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
   Shahrokh, Zahra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                   NUMBER OF SEQUENCES: 72
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Squence 477, Application US/09234340A

| Saguance 477, Application US/09234340A
| Patent No. 6466532
| GENERAL INFORMATION:
| APPLICANT: Genentech, Inc., Hsei, Vanessa
| APPLICANT: Genentech, Inc., Hsei, Vanessa
| APPLICANT: Bresta, Leonard G. APPLICANT: Bantrokh, Zahra
| APPLICANT: Sapato, Gerando A. TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES |
| TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES |
| ADDRESSEE: Genentech, Inc. | STREET: 1 DAN Way |
| CONTY: South San Francisco |
| STATE: California |
| COUNTY: USA |
| CONTY: South San Francisco |
| CONTY: CALIFORNIA |
| CONTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc., Heei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Withbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE: US/09/121,952
PILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07430
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07430
FILING DATE: 22-JAN-1998
APPLICATION NUMBER: 60/07467
FILING DATE: 20-FEB-1998
ATTORNEY.AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/POCKET NUMBER: 91085R4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.2
Matches 107; Conservative
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RESULT 11
US-08-908-469-12
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                                                                                                                                                                                                                                                                                                                                                                                        Score 506; DB 2; Length 108;
Pred. No. 3.6e-37;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/9/795,798 FILING DATE: 28-Peb-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: «Unknown»
TILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION»
RAPERENICALION NUMBER: 40,378
REFRENICE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/522-1994
TELEPHONE: 650/522-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION.
APPLICANT: Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 108 amino acids
TYPE: Amino Acid
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Best Local Similarity 89.8<sup>†</sup>
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                    JS-08-974-899-3
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                                                                                                                                                                                                       1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
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     Score 506; DB 2; Length 108;
Pred. No. 3.6e-37;
6; Mismatches 5; Indels
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Best Local Similarity 89.8%; Pred. No. 3.6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DS/MS-DOS SOFTWARE MINPERIN (Genentech) CURRENT APPLICATION DATA:

APPLICATION DATA: 21 May-2001
FILING DATE: 21 May-2001
PRIOR APPLICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07.APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY CARE TO THE CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-08-908-469-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
     90.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baca, Manuel
Query Match
Best Local Similarity 89.8
Matches 97; Conservative
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Humanized light chain variable region with signal OTHER INFORMATION: sequence NAME INFORMATION: sequence NAME SIGNAL 1 LOCATION: (1)...(19)
US-09-809-739-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGGGTKVEIKR 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 505; DB 2; Length 127;
Pred. No. 5.2e-37;
4; Mismatches 6; Indels
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
ITILE OF INVENTION: Method of Inhibiting Stenosis and
ITILE OF INVENTION: Restenosis
FILE REPERENCE: 1855.1065.003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR PELING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZUMAIN SALES AND SALES AND
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Sequence 1, Application US/07934373C
BACHI NO. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                              3-09-809-739-10
Sequence 10, Application US/09809739
Patent No. 6663863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Generatech, Inc. STREET: 1 DNA Way CITY: South San Francisco COUNTR: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%;
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Best Local Similarity 90.74
Matches 98; Conservative
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                                                                                                                     0; Gaps
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# Sequence 3, Application US/08146206C

# Patent No. 640713

# GENERAL INPORMATION:

# APPLICANT: Carter, Paul J.

# APPLICANT: Presta, Leonard G.

# TITLE OF INVENTION: Method for Making Humanized Antibodies

# NUMBER OF SEQUENCES: 26

# CORRESPONDENCE ADDRESS:

# ADDRESSEE Generatech, Inc.

# STREET: 1 DNA Way

# CITY: South San Prancisco

# STATE: California

# COUNTRY: USA
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                                                                 Query Match 90.0%; Score 504; DB 2; Length 109; Best Local Similarity 88.9%; Pred. No. 5.4e-37; Matches 96; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.0%; Score 504; DB 2; Length 109; Best Local Similarity 88.9%; Pred. No. 5.4e-37; Matches 96; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRI: USAN

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATPORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATPORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 07/715272
FILERPHONE 1650/225-1994
TELEPROMEY (225-1994
TELEPRAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: DO9 amino acide
TYPE: Amino Acid
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Linear
; TOPOLOGY:
US-08-437-642B-3
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April 13, 2006, 17:05:54 ; Search time 140.07 Seconds (without alignments) 543.993 Million cell updates/sec GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM protein - protein search, using sw model Run on:

US-10-727-737-2 560 1 DIOMIQSPSSLSASVGDRVT......QQHNEYPLIFGQGTKVBIKR 108 Title: Perfect score: Sequence:

Scoring table:

2166443 seqs, 705528306 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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		Score	486	481	481	479	479	478	476	475	474	473.5	471	471	470	464	463	463	462	461	461	460	458.5	458	458	456	455	455	455	452	452	452	451.5
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KVIK HUMAN QEPIHA HUMAN KVIE HUMAN KVIQ HUMAN QSRPEE HUMAN	KV1A HUMAN KV1X HUMAN	KVIJ HUMAN KVII HUMAN KVIC HUMAN	Q96PF6 HUMAN KV1T HUMAN KV5D_MOUSE
44444			244
108 108 108 234	108	117 117 108	116 109 108
80.4 79.8 79.8 79.1	78.4	77.1 77.0 76.8	76.4 75.6 73.6
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., WcKernan K.J., Malek J.A., Gunarate P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Schwultz J., Blockeon M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Marken A., Schein J.B., Jones S.J.M., Marra M.A.,
B. Marra M.A., Schein J.B., Jones S.J.M., Marra M.A.;
B. Marra M.A., Schein J.B., Jones S.J.M., Marra M.A.;
B. Marra M.A., Schein J.B., Jones S.J.M., Marra M.A.;
      1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                       61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 85.9%; Score 481; DB 2; Length 23: Similarity 85.2%; Pred. No. 6.2e-41; 92; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                    236 AA
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PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MRC; UNKNOWN 1.
Broather(cal protein; Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC005332; AAH05332.1; -; mENA.
HSSP; P01834; 1HEZ.
Ensembl; BNSG00000165245; Homo sapiens.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_WC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-8et; I.
                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                Q7Z3Y4_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                         Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                      0723Y4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                          82
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Mammalla, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                           23 DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #EDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dwulet F.E., O'Connor T.P., Benson M.D.;
"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
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HSSP; P80362; 1WTL.

SMR; P04430; 1-108.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:00005555; P:immune response; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR00356; Ig-v.

SMART; SM00406; IGv; 1.

PROSITE; PSS0835; IC_LIKE; 1.

Amyloid; Direct profein sequencing; Immunoglobulin domain;

Immunoglobulin V region.
                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                                                                           85.9%; Score 481; DB 1; Length 108; 83.3%; Pred. No. 2.5e-41; cive 9; Mismatches 9; Indels
                                                                                                             Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-3
                                                                                                           Score 486; DB 2; Length 23
Pred. No. 1.9e-41;
8; Mismatches 7; Indels
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00209; IG MHC; UNKNOWN 1.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11840 MW; CD3FD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA.
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                                                                                                             86.84;
                                                                                                                                 86.1%;
                                                                                                                                                   93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                               Similarity
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Best Local Similarity
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SEQUENCE
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Length 236;

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TISSUB-Primary B-Cells;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUBDENG R.L., Feligold B.A., Grouse L.H., Derge J.G.,

RIJAGER R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

As Expleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabey J., Helton B., Ketteman M., Madan A., Rouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Manterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodencration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC073763; AAH73763.1; -; mRNA.
SMR; QGGKX9; 23-236.
Ensembl; ENSG0000163245; Homo gapiens.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-8et; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences."
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SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
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NIH MGC Project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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"Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
"A. Exp. Med. 174.1639-1652 (1991).
EMBL, AF035044; AAD56280.1; -; mRNA.
PIR; PR0863; PR0863.
SMR; Q9UL70; 1108.
KPSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGQGTKLEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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rhes 10; Indels
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Last annotation update)
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                                                                                                                                                                      108 AA
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                               Created)
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InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                      OGUL70 HUMAN PRELIMINARY;
OGUL70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGMX9 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
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                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1660528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGKC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young D.C.;
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                                                                                                 RESULT 4

Q9UL70

DD 01-M

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10 0667
AC 0667
DT 065-
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DT 06-
DT
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                        Gaps
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                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                RFSGSGGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGTKVEIKR 130
                                                                                  Length 236;
                                                                                85.5%; Score 479; DB 2; Length 23
85.2%; Pred. No. 9.9e-41;
ive 8; Mismatches 8; Indels
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG WHC; UNKNOWN 1.
SEQUENCE 236 AA; Z5924 MW; PDE2093DC560CFF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                              QEPIH7_HUMAN PRELIMINARY;
                                                                                                                        92; Conservative
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Straubberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetow S.I., Warg J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Boask S.A., McKernan R.J., Malke J.A., Gunzarne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., W. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 IQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPSR
                                               MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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InterPro; IPR003599; IG.
InterPro; IPR0031010; Ig-like.
InterPro; IPR003006; Ig-MrC.
InterPro; IPR003596; Ig-V.
Pfam; PR07654; CL-set; I.
SWART; SW00400; IG; Z.
SWART; SW00400; IG:1, I.
SWART; SW00400; IG:1, I.
SWART; PS00939; IG LIKE; 2.
PROSITE; PS00939; IG LIKE; 2.
PROSITE; PS00939; IG MRG; UNRNOWN I.
SEQUENCE 236 AA; Z5751 MW; 5BFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO73791; AAH73791.1; -; mRNA.
SMR; QGGMM1; 24-236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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87.9%; Pred. No. 2e-40;
ilve 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snsembl; ENSG0000163245; Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Q9UL77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 87.9
les 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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                                                                    Straubberg R.L., Peingold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhar N.K.,

Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

By Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soarse M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Rapleton M., Soarse M.B., Bonaldo M.F., Carnhori P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tooshlyuk S., Carnhori P., Frange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Swancher B.D., Swancher B.D., Swancher B.D., Swancher B.D., Swancher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS
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                                          4EDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC Project;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034141; AAH34141.1; -; mRNA.
RHSSP; POLGO7; LAR2.
RHSSP; POLGO7; LAR2.
RNR; Q6PIH7; 23-236.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R SWART; SM00409; IG.
R SWART; SM00409; IG.1.
R SWART; SM00409; IG.1.
R PROSITE; PS00290; IG.LIKE; 2.
R SRQUENCE 236 AA; Z5603 MW; 8BG561106861213F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RPSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR
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Last annotation update)
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OGGMW1;
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NUCLEOTIDE SEQUENCE. MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

NCBI_TaxID=9606;

[1] NUCLEOTIDE SEQUENCE.

NCBI_TaxID=9606;

RESULT 7

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variable region (Fragment).
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PubMed=8436174;
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Buarchontoglires, Primates; Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                Wagner S.D., Luzzatto L.; "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                               Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.; "Human monoclonal striational autoantibodies isolated from thymic B lymphocytes of patients with myasthenia gravis use VH and VL gene segments associated with the autoimmune repertoire."; Eur. J. Immunol. 22:2231-2236(1992).
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"The primary structure of a monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                   Myosin-reactive autoantibodies in rheumatic carditis and normal
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-!- MISCELLANEOUS: The C region of this chain has the INV (3)
-!- MISCELLANEOUS: This is a Bence-Jones protein.
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Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 475; DB 2; Length 108;
Pred. No. 1e-40;
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    Last sequence update)
    Last annotation update)

                                                                        21in. Immunol. Immunopathol. 87:184-192(1998)
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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EMBL; AF035037; AAD56273.1; -; mRNA
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Ig kappa chain V-I region Hau.
Homo sapiens (Human).
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PROSITE; PS50835; IG_LIKE; 1.
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86.1%;
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PIR; S34083; S34083.
HSSP; P01607; IBWW.
SMR; Q9UL77; 1-108.
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10-MAY-2005
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
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                                                                                                                                                                                                                                                                                                                                                                                                SMAKI; SHOUTS, DESCRIPT, PS50835; IG LIKB; 1.
TO-SETUCTURE; Bence-Jones protein; Direct protein sequencing;
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84.3%; Pred. No. 1.3e-40;
ive 10; Mismatches 7; Indels
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                                                                                                                                                                                       PDB; 1F6L; X-ray; L=1-108.

GO; GO:0005576; C:extracellular region;

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; IG-like.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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J. Immunol. 161:2020-2031(1998).
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                   "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingool R.A., Grouse L.H., Derge J.G., Schuler G.D.,
Altschul R.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                             Manhelmer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                          Blaison G., Kuntz J.L., Pasquali J.L.;
Molecular analysis of V kappa III variable regions of polyclonal
"Humatoid factors during rheumatoid arthritis.";
Eur. J. Immunol. 21:1221-1227 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.6%; Score 473.5; DB 2; Length 107; 88.0%; Pred. No. 1.5e-40; tive 5; Mismatches 7; Indels 1;
                                                                                                                                                                                                   "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 107
107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AA
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                                                         somatic mutation.";
Eur. J. Immunol. 23:391-397(1993).
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U96396; AAB68785.1; -; mRNA
                                                                                                                                                                                                                                           Exp. Med. 174:1639-1652(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
SMART; SW00406; IGv; 1.
PR003TE; PS50815; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q502W4 HUMAN PRELIMINARY;
Q502W4;
Wagner S.D., Luzzatto L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, S16840, S16840.
PIR, S31977, S31977.
PIR, S34083, S34083.
PIR, S34086, S34086.
                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B49047; B49047
PIR; PH0867; PH0867
PIR; S16840; S16840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01607; 1BWW.
SMR; Q96SA9; 1-107.
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nes 95; Conserv
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                                                                                                                                       PubMed=1660528;
                                                                                                                                                                                                                                                                                                           PubMed=1903706;
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                                                                                                                                                                                Diamond B.;
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SEQUENCE
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Matches
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0502W4 HUM
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AC 0502W
DT 13-SE

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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McErana K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Schwinz J., Myers R.M., Schmin J.E., Jones B.D., Myers R.M., Schnin J.E., Jones S.J.M., Marxa M.A., Schail J.E., Jones S.J.M., Marxa M.A., Schail J.E., Jones S.J.M., Marxa M.A.,
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFAASSLQSGVPS
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EMBL; Y13057; CAA73500.1; -; mRNA.
Interpro; IPR003599; IG-11ke.
InterPro; IPR003596; Ig_V.
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InterPro; IRR007110; Ig-like.
InterPro; IRR007110; Ig-like.
InterPro; IRR003006; Ig-MHC.
InterPro; IRR003596; Ig-V.
InterPro; IRR003596; Ig-V.
InterPro; IRR00407; IG-1.
InterPro; IRR00407; IG-1.
INTERPRO; IRR00407; IG-1.
INTERPRO; IRR00407; IG-1.
IRR00406; IGV; I.
IRR00418; PSS0835; IG-IKR; 2.
IRR005ITE; PSS0835; IRR00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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84.3%; Pred. No. 6.6e-40;
clve 7; Mismatches 10
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SWR; Q502W4; 23-236.
Ensembl; ENSG0000163245; Homo sapiens.
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NIH MGC Project;
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Q65ZC8;
25-OCT-2004 (TEMBLFE). 28,
25-OCT-2004 (TEMBLFE). 28,
25-OCT-2004 (TEMBLFE). 28,
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PROTEIN SEQUENCE.
                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                               197 RFSGSGSGTDFTLTISSLOPDDFATYYCQQYSNYPLTFGGGTKLEIKR 244
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82.4%; Pred. No. 8.5e-40;
tive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97362799; Pubmed=9219263; DOI=10.1038/nbt0797-629;
                                                                                                                                                                                  10, Indels
                                                                                  244 244 247 AW; 4B1F17868338F2BF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kontermann R.B., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL, Y13056; CAA73499.1; -; mRNA.
InterPro; IPR007599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                          84.1%; Score 471; DB 2;
82.4%; Pred. No. 6.8e-40;
tive 9; Mismatches 10;
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(Rel. 01, Last sequence update)
(Rel. 48, Last annotation update)
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
NON_TER 1 1 1 1 NON_TER 244 244
SEQUENCE 244 AA; 26127 MW;
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21-JUL-1986 (Rel. 01, Last seq
21-SBP-2005 (Rel. 48, Last ann
1g kappa chain V-I region Lay.
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SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q652C9 HUMAN PRELIMINARY;
Q652C9;
                                                                                                                                                                                       Conservative
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                 Similarity
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                                                                                                                                            Query Match
Best Local Simi
Matches 89;
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P01605;
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ID KVIM HI
AC PO1605,
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DT 13-SEP-
DB 19 kapi
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,

Garson D., Solomon A., Mendez E., Frangione B.;

J. Immunol. 143:13864-3864(1989).

-!- MISCELLANEOUS: The second and third hypervariable regions of this chain are identical with those of the human POM V-III kappa chain, with which it shares certain idiotypic determinants.

-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.
                                                                                                                                                                                                                                       "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globuling [Lay/Pom) with shared idiotypic specificities."; Scand. J. Immunol. 5:677-684 (1976).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                          PROTEIN SEQUENCE OF 1-104.
MEDLINE=89215279; PubMed=2496160;
Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
Carson D., Solomon A., Mendez E., Frangione B.;
Structural and idiotypic characterization of the L chains of human
IgM autoantibodies with different specificities.";
J. Immunol. 142:3158-3163(1989).
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Complementarity-determining-3.
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PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
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SWR; PO1605; 1-108
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR00596; Ig-V.
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                                                                                                                                                                                                 MEDLINE=77038198; PubMed=824717;
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hes 87; Conservative
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TISSUB-LUNG;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peterg G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Tochman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Schalka U., Smailus D.E.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Menterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,

Menterfield Y.S. N., Krzywinski M.I., Shalska U., Smailus D.E.,

Menterfield Y.S. N., Krzywinski M.I., Shalska U., Smailus D.E.,

Menterfield Y.S. N., Krzywinski M.I., Shalska U., Smailus D.E.,

Menterfield Y.S. N., Krzywinski M.I., Shalska U., Smailus D.E.,

Menterfield W. Anderson M. Indital analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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InterPro; IPR003110; Ig-11ke.
InterPro; IPR003106; Ig-MHC.
InterPro; IPR003156; Ig-V.
Pfam; PF07654; Cl-set; I.
SMART; SM00406; IGV; I.
FROSITE; PS05035; IG-LIKE; 2.
PROSITE; PS06395; IG-MHC; UNKNOWN_1.
Immunoglobulin domain.
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
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NIH MGC Project;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56556; AM566256.1; -; mRNA.
HSSP; PO1834; 1HEZ.
SWR; Q72473; 222-234.
                                                                                                                                        01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                    234 AA
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Job time : 141.07 secs
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RESULT 15

O72473 HUMAN

ID Q72473 HUMAN PRELIMINARY;

AC 01-OCT-2003 (TYEMBLrel. 25,
DT 01-OCT-2003 (TYEMBLrel. 26,
DT 01-OCT-2003 (TYEMBLrel. 26,
DT 01-MAR-2004 (TYEMBRREL. 26,
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Best Local S
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 13, 2006, 17:14:06; Search time 23.1092 Seconds (without alignments) 449.666 Million cell updates/sec Run on:

1 DIQMTQSPSSLSASVGDRVT.....QQHNEYPLTFGQGTKVEIKR 108 US-10-727-737-2 560 Title: Ferfect score: Sequence:

BLOSUM62 Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pir 80:* 1: pir1:* 2: pir2:* 1: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

	Description	Ig kappa chain V-J	kappa	Ig kappa chain - h	kappa chain		Ig kappa chain V-J	kappa	kappa chain	kappa	kappa c	lambda	kappa	kappa	light c		lambda	kappa chain	chain 1	lambda chain	kappa	light	kappa chain	kappa chain	kappa chain pr	kappa chain	kappa	kappa	kappa c	
SUMMARIES	01	840333	B49047	S40369	846371	S40349	840367	S19674	840331	S40352	840336	836264	S40334	KIHUBN	846372	169017	836275	S46376	K1HUHU	836277	S38646	826345	S31998	840353	S04574	844122	840318	840316	305	S36279
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	Query Match	88.0	87.5	87.5	•	87.0	87.0				86.5	86.2	86.2	85.9	85.5	85.4	85.1	85.0		•		84.5	84.5		84.5			83.8	83.5	83.2
	Score	493	490	490	489	487	487	486	486	486	484.5	483	483	481	479	478	476.5	476	474	474	474	473	473	473	473	472	471	469	467.5	466
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Ig kappa chain - h	Ig kappa chain - h	Ig kappa chain V r	Ig lambda chain V			Ig kappa chain - h									Ig kappa chain V-J
847182	S31981	852793	836269	KTHOLY	S34007	S47183	840370	840350	\$11240	KIHUGL	K1HUKU	S52789	KIHUWS	I39154	S46370
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108	109	129	107	108	108	107	122	125	127	108	108	129	108	108	120
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						462.5 82.6									

ALIGNMENTS

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A;Residues: 1-125 «KLE»
A;Residues: 1-125 «KLE»
A;Residues: 1-125 «KLE»
C;Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:9441354; PIDN:CAA51111.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IPM>
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                              C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                         C,Accession: S4033
R;Actession: S4033
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 88.0%; Score 493; DB 2; Length 125; 1 Similarity 86.9%; Pred. No. 3.2e-34; 93; Conservative 9; Mismatches 5; Indels
                                                                                                                                                                                                             A;Accession: S40333
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
Ig kappa chain V-J region - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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B49047

If kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme C;Species: Homo sapiens (man)
R;Victor, R;D:; Pascual, V; Williams, C.L.; Lennon, V.A.; Capra, J.D.
R;Victor, K.D.; Pascual, V; Williams, C.L.; Lennon, V.A.; Capra, J.D.
R;Victor, Human monoclonal striational autoantibodies isolated from thymic B lymphocytes c
A;Reference number: A49047; MUID:92387224; PMID:1516616

A; Accession: B49047

A;Status: preliminary

A;Molecule type: nucleic acid A;Roseidues: 1-108 <VIC> A;Crose-references: UntrROT:096SA9; UNIPROT:09UL77; UNIPARC:UPI0000176B44 A;Experimental source: thymic B lymphocytes A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209) C;Superfamily: immunoglobulin vegion; immunoglobulin homology <IMM>

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A;Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PII CS.Superfamily: immunoglobulin vegion; immunoglobulin homology C;Koywords: heterotetramer; immunoglobulin nemorg;Koywords: heterotetramer; immunoglobulin homology <IMM> F;33-107/pomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 IQLIQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPKLLIYAASSLQSGVPS 77
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                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 19-May.1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: 840349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bir. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
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C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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R; Klein, R.; Jaentchen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: S40312; MUID:94080891; PMID:8258341
A; Accession: S40367
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-127 < KLE>
      68 RFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYFPPYTFGQGTKLEIKR 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 FSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 487; DB 2; Length 127;
Pred. No. 1e-33;
5; Mismatches 8; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 487;
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A, Status: preliminary; translation not shown
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A; Residues: 1-125 <KLE>
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C;Species: Homo sapiens (man)
C;Date: 27-Jan.196 Hacquence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: 846311, 838645
R;Bensimon, C.; Chastagner, P.; Zouali, M.
BMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autcantibodies undergo essentially primary V(chi) gene : A;Reference number: 846369; MUID:94313975; PMID:8039491
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40369
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-2271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40316;
A;Accession: S40369
                                                                                                                                                DIQMIQSPSTLSASVGDRVIITCRASRSISTWLAWYQQKPGKAPKLLIYKASTLESGVPS
                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLOSGVPS
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Score 490; DB 2; Length 108;
Pred. No. 5e-34;
4; Mismatches 8; Indels
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Pred. No. 6.5e-34;
9; Mismatches 5; Indels
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86.1%; Pred. No. 5.9e-34;
ive 7; Mismatches 8;
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87.5%;
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Best Local Similarity 85.5%;
Matches 94; Conservative
                                                      96; Conservative
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                           Best Local Similarity
Matches 96; Conserv
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Best Local Similarity
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A, Molecule type: mRNA
A, Residues: 1-117 <BEN>
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   Query Match
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A;Cross-references: UNIPARC:UP1000116156; EMBL:X72446; NID:9441360; PIDN:CAA51114.1; PII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;31-105/Domain: immunoglobulin homology <IMM>
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Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Now sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36264
E;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Feference number: S36256; MUID:93178448; PMID:7679990
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A,Residues: 1-107 <GRL>
A,Residues: 1-107 <GRL>
A,Cross-references: UNIPARC:UPI0000118DF4; EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID: C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                     21 DIOMTOSPSSLSASVGNRVTITCRASOGISNYLAWYQQKPGKVPKLLIYAASTLOSGVPS
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R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
A;Itle: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; WUD:94080891; PMID:8258341
A;Accession: $40336
A;Status: preliminary; translation not shown
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                                                                                     Length 131;
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                                                                                     Score 486; DB 2; Length 13
Pred. No. 1.3e-33;
6; Mismatches 8; Indels
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86.0%; Pred. No. 1.9e-33;
ive 9; Mismatches 6; Indels
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C; Keywords: heterotetramer; immunoglobulin P;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                  cch 86.8%;
al Similarity 87.0%;
94; Conservative
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Best Local Similarity 86.0
Matches 92; Conservative
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Matches 96; Conserv
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A; Residues: 1-124 < KLE>
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R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
                     J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on
A:Reference number: $1963; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:9441350; PIDN:CAA51109.1; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
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A;Residues: 1-131 <KIE>
ZCOSB-references: UNIE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Cibate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cibate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Cibacesion: 840552
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
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3;Klein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3246-3271, 1993

B.Title: Expressed human immunoglobulin chi genes and their hypermutation.

B.Reference number: S40312; MUID:94080891; PMID:8258341
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86.1%; Pred. No. 1.1e-33;
ive 8; Mismatches 7; Indels
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C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Accession: 840331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
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1es 93; Conservative
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IG light chain variable region (VJ) - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: S46372
R; Bensimon, C.; Chastagner, P.; Zouall, M.
EMBO J. 13, 2951-2962, 1994
A; Fitle: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene reas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP10000113F9C; GB:S77140; NID:g913352; PIDN:AAB34102.1; PID:c;Ganetics:
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
                                                                                                                                       1 DIQLIQSPSSISASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60
                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
9; Indels
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9; Mismatches
    90; Conservative
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A: Residues: 1-107 < RES>
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;1-23/Region: framework I
F;16-90/Domain: immunoglobulin homology <IMM>
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1 EIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo Bapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S40334

K; Klein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A; Title: Expressed human immunoglobulin chi genes and their hypermutation.

A; Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mol. Immunol. 23, 73-78, 1986
A. Tittle: Polymorphism in a kappa I primary (AL) amyloid protein (BAN)
A;Reference number: A01878; MUID:86174817; PMID:3083240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RESGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                61 RPSGSGSGTDFTLTISSLOPEDFATYYCQQHNEYPLTFGQGTKVEIK 107
                                                                                                                                                            RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNYPLTFGGGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 86.2%; Score 483; DB 2; Length 132; Best Local Similarity 85.2%; Pred. No. 2.3e-33; Matches 92; Conservative 7; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-132 «KLE»
A;Cross-references: UNIPARC:UP10000176CA9; EMBL:X7244
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
P;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 1-108 <DWU>
A,Cross-references: UNIPROT:P04430; UNIPARC:UPI000012E150
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83.3%; Pred. No. 2.8e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: S40334
A, Status: preliminary; translation not shown
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23-88/Disulfide bonds: #status predicted
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: mRNA
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RESULT 13

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61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPITFGQGTKVLIK 107

Search completed: April 13, 2006, 17:19:34 Job time : 23.1092 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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¹ DIQMTQSPSSLSASVGDRVT.....QQHNEYPLTFGQGTKVEIKR 108 Sequence:

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Scoring table:

2443163 of hits satisfying chosen parameters: Total number

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp2003as:*geneseqp2003bs:* geneseqp2001s:*geneseqp2002s:* A Geneseq 21:* 1: geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20048:*

geneseqp2005s:*

SUMMARIES

	Description	Aaw62017 Light cha	Aaw63529 Humanised	Aay82343 Humanised	Adg38990 Humanised		7	-	Adf11669 anti-CD11	Aay29449 Human lig	Aay77752 Human lig	Aab30309 Human lig	Abul3786 Human lig	Human	2 Human	Aab46020 Human MUC	Aaw70622 Human con	Aay82345 Human con	Abp61191 Human ant	Human	Human	Adp79572 Human kap	Aau74544 Human sub	Aea38745 Human VL	Aae28149 Human con
COLUMNICO	ΙΙ	AAW62017	AAW63529	AAY82343	ADG38990	ADR03365	ADW38457	ADX80645	ADF11669	AAY29449	AAY77752	AAB30309	ABU13786	ABU59499	AAE39082	AAB46020	AAW70622	AAY82345	ABP61191	ADG38991	ADR03366	ADP79572	AAU74544	AEA38745	AAE28149
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de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.6	97.6	9.76	97.6	97.6	97.6	91.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4	90.4
	Score	260	260	260	260	260	560	260	560	546.5	546.5	546.5	546.5	546.5	546.5	512	206	206	206	206	206	206	206	506	206
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Aau09917 Light cha Abg75526 Humanised Ad123195 Human ant			Adj88008 Human var Adn12054 Variable Adp43328 Human mon ahi18679 anrihodv	Human Human Amino	Adm47073 Mouse ant Aab45993 Human MUC Ado36411 Intracell Aea41087 Germline
AAU09917 ABG75526 ADL23195	AAR40956 AAB45991 ADW04801	AAB60400 AAB61585 ADE71454	ADJ88008 ADN12054 ADP43328	AAW27543 AAB46004 AAY56737	ADM47073 AAB45993 ADO36411 AEA41087
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ALIGNMENTS

Complementarity determining region; light chain variable region; humanised antibody; MFMA4F(ab)-8; anti-CD11a antibody; MFMA4F(ab)-8; anti-CD11a antibody; human CD11a I domain; MFMA4 epitope; alpha subunit; lymphocyte function-associated antigen 1; LFR-1; immunoassay; in vivo imaging; diagnosis; CD11a-associated disease. Light chain variable region of humanised anti-CD11a antibody AAW62017 standard; peptide; 108 AA (first entry) 01-OCT-1998 AAW62017; AAW62017

Homo sapiens. WO9823761-A1.

97WO-US019041. 20-OCT-1997; 04-JUN-1998.

96US-00757205. (GETH) GENENTECH INC. 27-NOV-1996;

Presta LG; Jardieu PM,

WPI; 1998-322737/28.

New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease.

Claim 9; Page 48; 66pp; English.

The present sequence represents the light chain variable region of a humanised anti-CD11a antibody that binds specifically to the human CD11a fonain (WEM24 epitope). CD11a refers to the alpha subunit of lymphocyte function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-CD11a antibodies are used to determine presence of CD11a in usual immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-sasociated diseases (typically immune responses and inflammation such as psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,

²⁴⁴³¹⁶³ segs, 439378781 residues Gapop 10.0 , Gapext 0.5 Searched:

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This sequence represents the light chain of the humanised antibody MFM24, and was used to produce a mutant of the invention. The mutants are of a species-dependent antibody (Ab), and have an amino acid substitution in a variable region of the Ab, and binding affinity for an antigen (Ag) from a non-human mammal at least 10 times stronger than for the wild type Ab against the Ag. The mutant antibodies are particularly intended for administration to a non-human mammal in precilinical studies (e.g. of infection, immunity, haematopoiesis or transplantation). They can also be used diagnostically (to identify specific proteins) or therapeutically, e.g. where directed against Colla (lymphocyte function-associated antigen). Or intercellular adhesion molecule-1 against a wide variety of inflammatory or autoimmune diseases, malignancies, transplant rejection, human immune deficiency virus infection and tumour cell invasion.

C conversion to the mutant form allows useful antibodies to be produced from antibodies which normally have affinity for non-human analogues of the Ag too low to be of any use
                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody mutant production; species-dependent antibody; malignancy; infection; haematopolesis; lymphocyte function-associated antigen-1; intercellular adhesion molecule-1; inflammatory disease; CDlla; therapy; autoimmune disease; transplant rejection; tumour cell invasion; human immune deficiency virus infection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutants of species-dependent antibodies with affinity for non-human mammalian antigon - greater than for parent antibody, particularly used for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies directed against CD1a.
                                                                                                                        1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                           DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                        Gaps
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                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                     Length 108;
                                                                                      Indels
                                                   Score 560; DB 2;
Pred. No. 4.9e-33;
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                                   Disclosure; Page 53; 71pp; English.
                                                                                                                                                                                                                                                                                                                      AAW63529 standard; protein; 108 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised MHM24 light chain.
                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1998 (first entry)
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-322726/28.
                                                                  Sest Local Similarity
                  Sequence 108 AA;
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                                                                                     Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                         AAW63529;
                                                   Query Match
                                                                                                                                                                                                                                                                                     RESULT 2
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The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated with inflammatory hich is involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (1) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen-1 (IrA-1; CD11a/CD18), e.g. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, rinilammatory bowel disease, eczema, systemic lupus erythematosus, rinilammatory bowel disease, eczema, systemic lupus erythematosus, rinilammatory bowel disease, eczema, systemic lupus erythematosus, rinilamatory bowel disease, eczema, systemic lupus erythematosus, rinilamatory bowel disease, eczema, systemic lupus erythematosus, of undour pretreatment; (1) when labeled, to detect CD11a; (11) for unmour pretreatment; (11) when labeled, to detect CD11a; (11) for catain about the same activity in adhesion and mixed lymphocyte response sasys as the murine antibody winka for preventing adhesion between Jurkat cells (expressing LFA-1) and normal epidermal cantiocytes that express ICO 0.09 nM for preventing adhesion between Jurkat cells (expressing LFA-1) and normal epidermal canting the humanised version of MHM-1 (intracellula antibody humanised version of MHM-1 (intracellula antibody entry erity with the humanised antiperson entry erity and variable region of the humanised antiperson entry ent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-CD11a antibody, useful for treating or preventing e.g. inflammation and transplant rejection, contains human heavy variable region complementarity determining regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitunour; antiviral; inflammation; immunological response; LFA-1; lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
                                                                                                                                              DIQMTQSP8SLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.
                                                          Gaps
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                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
     Length 108;
                                                     0; Indels
100.0%; Score 560; DB 2; 100.0%; Pred. No. 4.9e-33;
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          AAY82343 standard; protein; 108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                           Best Local Simitaricy .... Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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  Query Match
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                                                                                                                                                                                                                                                                                                                                               RESULT 3
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(CD) Its antibody having specificity to human CD11a I-domain or CD11a with a ked value of not more than 1x10-8 M, or concentration for 50 % inhibition (ICSO) (aM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)—I. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody by culturing the cell so that the antibody is useful for determining the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region; VL; cluster of differentiation 11a; mixed lymphocyte response assay; Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule; ICAM-1; lymphocyte function-associated antigen I mediated disorder; psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; prodrug activating enzyme; humanised.
                                                                                                                                                                                                DIÓMTÓSPSSLSASVGDRVTITCRASKTISKYLAMYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohns disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
                                                                                                                                                         DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised Mouse anti-CD11a antibody light chain variable region.
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                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNRYPLTFGQGTKVBIKR 108
                                                                                                                                                                                                                                                             RFSGSGGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVBIKR 108
                                                                        Length 108;
                                                                                                                  0; Indels
                                                                          ; Score 560; DB 3;
; Pred. No. 4.9e-33;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                               ADG38990 standard; protein; 108
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97US-00974899.
99US-00420745.
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                                                                                               100.08;
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                                                                      Query Match
Best Local Similarity 100.
Matches 108; Conservative
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                                       Sequence 108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
-CD11a Ab
                                                                                                                                                                                                                                                                                                                                                                                                                      ADG38990;
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as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the light chain variable region (VL) of the humanised mouse anti-CD11a I domain monoclonal antibody MHM24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDlla antibody; human immunodeficiency virus infection; HIV infection; rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory bowel disease; Crohn's disease; psoriasis; adult respiratory distress syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SLE; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis; opp, CNS inflammatory disease; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak; B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia; graft versus host disease; cancer; gene therapy; murine anti-human CDlla monoclonal antibody; MHM24; variable light chain; murine anti-human CDlla monoclonal antibody; MHM24; variable light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody mutant of a species-dependent antibody, useful for treating and preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.
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                                                                                                                                                                                                                                                                        1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIXSGSTLQSGVPS
                                                                                                                                                                                                                                                     1 DIOMIOSPSSISASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised MHM24 F(ab)-8 antibody variable light chain protein.
                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                            Length 108;
                                                                                                                                                                                                              Indels
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0
                                                                                                                                                                        100.0%; Score 560; DB 8;
100.0%; Pred. No. 4.9e-33;
live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR03365 standard; protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-2003; 2003US-00727737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1996; 96US-0031945P.
20-NOV-1997; 97US-00975329.
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                                                                                                                                                                                          Local Similarity 100 hes 108; Conservative
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                                                                                                                                       Sequence 108 AA;
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR03365
                                                                                                                                                                          Query Match
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Sequence 108 AA;

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for treating and preventing infectious diseases such as human immundeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel disease such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, a llergic diseases such as eczema and asthma, autoimmune diseases such as rheurits, systemic lupus erythematosus (SLB), diabetes mellitus, Reynaud's syndrome, immunological diseases such as mellitus, Raynaud's inflammatory disorder, skin hypersensitivity disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD11a monoclonal antibody (MHM24) F(ab)-8 variable light chain protein. This sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 560; DB 8; Length 108; 100.0%; Pred. No. 4.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; CD11a; light-chain variable region; heavy-chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADW38457 standard; protein; 108 AA
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Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 108 AA;
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Recombinant human CD11a monoclonal antibody and its preparation and
                                                                                                                         (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI
                                                                                                                                                                             Claim 1; Page 14; 16pp; Chinese.
                                                                                                  20-FEB-2002, 2002CN-00110866
                                                                                                              20-FEB-2002; 2002CN-00110866.
                                                                                                                                                                  medicinal composition.
                                                                                                                                                WPI; 2004-169719/17.
                                                                                                                                    Wang H, Wang J;
                                                               Homo sapiens
                                                                           CN1439651-A
                                                                                       03-SEP-2003
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The invention relates to a method of purifying a protein which comprises a CH2/CH3 region by protein A affinity chromatography. The method involves reducing the temperature of a composition comprising the protein and one or more impurities subjected to protein A affinity chromatography to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably the protein is antibody. The antibody is selected from Trastuzumab, the manized CD11a antibody, and humanized VEGF antibody. Preferably, the antibody binds HER2 antigen, where the antibody is Trastuzumab or humanized 2C4. The protein is an immunoadhesin, specifically a TNP receptor immunoadhesin. The methods are useful for specifically a TNP receptor immunoadhesin. The methods are useful for specifically chromatography and for reducing leaching of protein A affinity chromatography. The current sequence represents the variable light chain amino acid sequence of CD11a.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Protein purification; leaching; protein A affinity chromatography; CD11a;
                                                                                              1 DIQMIQSPSSLSASVGDRVIITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60
                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purifying a protein, e.g. antibody or immunoadhesin, comprises reducin the temperature of a composition subjected to protein A affinity chromatography to 3-20 degrees C, where protein A leaching is reduced.
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                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                              61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
 Length 108;
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                                                                                                                                                                                                                                                                                                                                                                                  Humanized CD11a variable light chain amino acid sequence,
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100.0%; Pred. No. 4.9e-33;
ive 0; Mismatches 0; Indels
                                   Indels
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 Score 560; DB 8;
Pred. No. 4.9e-33;
                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 5; 27pp; English
                                                                                                                                                                                                                                                                         ADX80645 standard; protein; 108 AA.
 100.0%;
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Matches 108; Conservative
                                   Matches 108; Conservative
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody
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1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS 60

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The present invention relates to a recombinant monoclonal antibody for human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID No.5 in 1ight-chain variable region and the amino acid sequence shown by SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its bloactivity and the expression in host cell are greatly increased. The DNA molecule for coding the antibody, its preparation process and the medicinal composition containing it are also disclosed. The present sequence represents a light chain variable region of human CD11a.

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61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                             AAY29449 standard; protein; 109 AA
                                                                                      AAY29449;
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                                                    AAY29449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mixture containing a host cell protein. This method comprises subjecting the mixture containing a host cell protein. This method comprises subjecting the mixture to a non-affinity purification followed by high-performance cangential flow filtration (HPTPP) and isolating the protein in a purity containing less than 100 parts/million (ppm) of the host cell protein, where the method of the invention is useful for purifying a target protein from a mixture containing a host cell protein, and is useful for incorporating the isolated protein into a pharmaceutical formulation. Containing the method of the invention are useful in a pharmaceutic purposes. The method of the invention is efficient in purifying a target protein from a mixture containing a host cell protein, cand may also be effectively performed at low cost. The current sequence represents the anti-Chila rhuwab light chain amino acid sequence.
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The invention relates to a method for purifying a target protein from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purifying target protein from mixture containing host cell protein involves subjecting mixture to non-affinity purification, high-performance tangential flow filtration and isolating purified protein.
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                                                                                                                                                                                                                      Purifying; target protein; non-affinity purification;
high-performance tangential flow filtration; HPTFF; pharmaceutical;
diagnostic; therapeutic; antibody.
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                                   RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
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                                                                                                                                                                                                 anti-CD11a rhuMAb light chain amino acid sequence #SEQ ID 3
                                                                                                                                                                                                                                                                                                                                                                                                                         Van Reis R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 3; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         Lebreton B,
                                                                                                                          ADF11669 standard; protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                 25-APR-2003; 2003WO-US013054.
                                                                                                                                                                                                                                                                                                                                                                         26-APR-2002; 2002US-0375953P.
                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-043096/04.
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                                                                                                                                                                          26-FEB-2004
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Matches 108;
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                                                                                                                                                                                                                                                                                                                          11-DEC-2003
                                                                                                                                                                                                                                                                           Synthetic.
                                      61
                                                                                                                                                 ADP11669;
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conjugates of nonproteinaceous polymers with antibody fragments, used
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                                                                                                                         anti-IL-8 monoclonal antibody; interleukin 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zapata
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                                                                                                                                                     diagnosis; inflammatory disorder; conjugate; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.6%; Score 546.5; DB 2
98.2%; Pred. No. 4.6e-32;
ive 1; Mismatches 0
                                                           Human light chain kappa-I consensus framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 29; 360pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leong SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00012116.
98WO-US003337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00121952.
98US-00122513.
                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US001081.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koumenis I,
                                                                                                                      Antibody; humanised;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-469134/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 109 AA;
                                                                                                                                                                                        fusion protein.
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                     W09937779-A1
05-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-1998;
20-FEB-1998;
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ID AAY7
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AAY77752 standard; protein; 109 AA.

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1 DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYSGSTLQSGVPS DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAMYQQKPGKAPKLLIYSGSTLQSGVPS

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61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108

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99US-00234340.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 109 AA;
                                     Homo sapiens
                                                                                                       20-FEB-1998;
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                                                                                                                              21-FEB-1997;
                                                                                                                                         22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                         US6133426-A.
                                                                                 17-0CT-2000
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                                                                              Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.5V11N35A;
inflammatory disorder; adult respiratory distress syndrome; chimeric;
affinity purification; 6G4.2.5.
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 64-2.5VINN35A light chain, and amino acids 24-253 of the humanized anti-IL-8 664.2.5VINN35A heavy chain. The anti-IL-8 MAbs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-In-8 MAb can be associated in a vector with another gene encoding another protein or protein fragment to produce a fusion protein which can make isolation and/or purification of the protein an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule encodes a polypeptide which is an anti-
interleukin-8 monoclonal antibody or antibody fragment useful for the
production of anti-interleukin-8 monoclonal antibodies or fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 SRPSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.6%; Score 546.5; DB 3; Length 109; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human light chain kappal consensus framework SEQ ID NO: 47.
                                                        Human light chain k1 consensus framework,
                                                                                                                                                                                                                                                                               Gonzalez TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB30309 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                        Example, Fig 29, 188pp, English.
                                                                                                                                                                                                98US-00027449.
                                                                                                                                                                                                                     97US-0038664P.
98US-0074330P.
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.2
Matches 107; Conservative
                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                               Leong SR,
                                                                                                                                                                                                                                                                                                     WPI; 2000-181809/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sasier process
                                                                                                                             Homo sapiens
                                                                                                                                                                                               20-FEB-1998;
                                                                                                                                                                                                                      21-FEB-1997;
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                                 06-JUN-2000
                                                                                                                                                 US6025158-A.
                                                                                                                                                                        15-FEB-2000
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                                                                                                                                                                                                                                                                             Presta LG,
            AAY77752;
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The present invention provides a number of humanised monoclonal anti-IL-8 anti-bodies which can be used in the diagnosis and treatment of inflammatory disorders, including adult respiratory distress syndrome, septite shock, multiple organ failure, bacterial pneumonia and inflammatory bowel disease. The present sequence comprises one of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; respiratory; scute lung injury; polyethylene glycol; PEG; lung injury; adult respiratory distress syndrome; AEDS; sathma; inflammatory disease; psoriasis; sclerosis; ischaemic peperfusion disorder; stroke; multiple sclerosis; meningitis; osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis; alcoholic hepatitis; cystic fibrosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized anti-interleukin 8 monoclonal antibody variant useful for treating inflammatory disorders, such as adult respiratory distress syndrome, hypovolemic shock and ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mAb;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.6%; Score 546.5; DB 3; Length 109; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0; Indels 1.
adult respiratory distress syndrome; multiple organ failure; bacterial pneumonia; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human light chain kappal consensus framework sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 161-162; 240pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gonzalez TN
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                                                                                                                                                                                                                                                                                                                                             98US-00026985.
                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0038664P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Presta LG, Leong SR,
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The invention relates to treating acute lung injury in a mammal, comprising administering to the mammal an effective amount of a conjugate copy and antibody fragment covalently attached to 1 or 2 polyethylene cylycol (FBG) molecules, where the antibody fragment is a F(ab') 2 comprising: (a) first chain that is either a light chain or a heavy chain opposite the first hight chain or a light chain opposite the first heavy chain; (C) a second chain that is either a heavy chain; and (d) a second chain that is either a heavy chain; and (d) a second chain that is either a heavy chain; where every EBG molecule is covalently attached to a first cysteine residue in the first con second chain that would ordinarily form a disulphide bridge with a second cysteine residue in the first or second opposite chain, where the second cysteine residue in the first or second opposite bridge is avoided by substitution of another amino acid cresidue for the second cysteine residue in the first or second opposite chain, where the F(ab') 2 comprises an antigen binding site that binds to human interleukin-8 (IL-8), and where the apparent size of the conjugate chain, where the F(ab') 2, and where the apparent size of the conjugate conjugate in a mammal and inflammatory diseases syndrome murine monoclonal antibodies 5.12.14 or 642.5. The method is useful for treating lung injury, including adult respiratory distress syndrome conformatory bowel disease, psoriasis and sclerosis, meningtis, consensed and disorders isted in the specification. The present sequence conforms and disorders listed in the specification. The present sequence is represente a human antibody a sequence fibrored arthritis, and where the specification. The present sequence is the comparison with the monoclous has a sequence in the sequence is the specification. The present sequence
                                                                                                                                                                                                                                                                                                Treating acute lung injury in mammal by administering to mammal a 500 kD conjugate comprising P(ab') 2 antibody fragment that binds to human interleukin-8, covalently attached to one or two polyethylene glycol
                                                                                                                                                                                                    Zapata G;
                                                                                                                                                                                                  Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Example G; Fig 29; 259pp; English
                    98US-0074330P.
98US-0075467P.
98US-0094003P.
98US-0094013P.
                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                    WPI; 2003-138230/13
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                                               20-FEB-1998;
24-JUL-1998;
24-JUL-1998;
                       22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                 molecules
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                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLIYYSGSTLESGVP
                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                             1; Gaps
                                                                                                                                                                      60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 108
                                                                                                                                                                                                61 SRFSGSGSGTDFTLTISSLQPEDPATYYCQQHNEYPLTFGQGTKVEIKR 109
  Length 109;
                                           0; Indels
    9
  97.6%; Score 546.5; DB 6; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0;
Query Match
Best Local Similarity 98.2
Matches 107; Conservative
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Human light chain kappal consensus framework. ABU59499 standard; protein; 109 AA. 22-APR-2003 (first entry) ABU59499; ABU59499

Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5; inflammatory disorder; psoriasis; atopic dermatitis; sclerosis; systemic scleroderms; inflammatory bowel disease; Crohn's disease; ulcerative colitis; ischaemia; reperfusion; myocardial infarction; stroke; adult respiratory distress syndrome; rheumatoid arthritis; alcoholic hepatitis; acute lung injury; asthms; cerebral oedema; myocardial ischaemia; cranial trauma; asphyxia; Behcet's disease; dermatomyositis; polymyositis; multiple sclerosis; meningitis; encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma; autoimmune disease; Sjogren's syndrome; vasculitis; septicaemia; central nervous system inflammatory disorder; sepsis; sarcoidosis; inflammation of the lung; human.

JS6458355-B1

31-OCT-2002

98US-00121952. 24-JUL-1998;

98US-0074330P. 22-JAN-1998;

20-FEB-1998;

(GETH) GENENTECH INC.

Shahrokh Z, Presta L, Leong S, Koumenis I, Hsei V,

Treating inflammatory disorder in a mammal, involves administering a conjugate of polyethylene glycol and a single antibody fragment comprising antigen binding site that binds to human interleukin-8, to

Example 3G; Fig 29; 259pp; English.

The invention relates to treating an inflammatory disorder in a mammal, comprising administering to the mammal, an effective amount of a conjugate of a single antibody fragment (e.g. the heavy or light chains of the humanised mouse monoclonal antibodies 5.12.14 and 664.2.5, which also have their intramolecular disulphide bridges ablated by substitution mutations covalently attached to one or two polyethylene glycol (PBG) molecules. The antibodies comprise an antigen binding site that binds to human interleukin-8 (IL-8), and the apparent size of the conjugate is at least 500 kbs. The method is useful for treating an inflammatory disorder e.g. ischaemic reperfusion disorder such as surgical tissue reperfusion injury, myocardial ischaemia or myocardial infarction, or hypovolemic shock, in a mammal e.g. human. The method is useful for treating injury, myocardial ischaemia or myocardial infarction, or hypovolemic shock, in a mammal e.g. human. The method is useful for treating calcroderma and sclerosis, responses associated with inflammatory bowel disease, ischaemic reperfusion disorders, myocardial ischaemic conditions, cerebral codema secondary to stroke, cranial trauma, asphyria, adult respiratory distress syndrome, caute-lung injury, Behcet's disease, dermatomycostis, polymyositis, multiple sclerosis, dermatitis, encephalitis, polymyositis, multiple sclerosis, cantible organ injury syndrome secondary to septicaemia or trauma, alcoholic hepsitis, bacterial pneumonia, antigenential premumania, antigenential premumania, antigenential pneumonia, antigenential premumania, antigenenti mediated diseases including glomerulonephritis, sepsis, sarcoidosis, immunopathologic responses to tissue/organ transplantation, inflammations of the lung, inflammatory bowel disease such as ulcerative colitis and asthma. The present sequence represents the light or heavy chain of human 1gG, used to design the humanising mutations in the two mouse antibodies

Sequence 109 AA;

ï Gaps ; 97.6%; Score 546.5; DB 6; Length 109; 98.2%; Pred. No. 4.6e-32; ive 1; Mismatches 0; Indels 1; Best Local Similarity 98.2 Matches 107; Conservative Query Match

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60 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel conjugates comprising antibody fragments covalently attached to nomproteinaceous polymer molecules. The invention is useful for treating interleukin (IL) a mediated diseases or disorders such as inflammatory diseases, acute lung injury e.g. adult respiratory distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial infarction, hypoolemic shock, inflammatory bowel disease e.g. uncertained colitis, bacterial pneumonia and asthma. The invention is also useful as a reagent in an animal model system for in vivo study of the biological succious of the antigen recognised by the conjugate. The present sequence is used in the exemplification of the invention
   59
                                                                                                                                                                                                                                                                                                                 Interleukin-8 mediated disease; adult respiratory distress syndrome; IL; bacterial pneumonia; inflammatory bowel disease; hypvolemic shock; ARDS; ulcerative colitis; ischaemic reperfusion injury; myocardial infarction; acute lung injury; hilammatory disease; asthma; antibody; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel conjugates comprising antibody fragments covalently attached to nonproteinaceous polymer molecules, useful for treating inflammatory diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
                   DIQMTQSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zapata G;
                                                                 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNBYPLTFGQGTKVEIKR 108
                                                                                      SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGGGTKVEIKR 109
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                                                                                                                                                                                                                                                                                   Human light chain kappaI consensus framework protein.
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98.2%; Pred. No. 4.6e-32;
ive 1; Mismatches 0;
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                                                                                                                                                                                  AAE39082 standard; protein; 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0074330P.
98US-0075467P.
98US-0094003P.
98US-0094013P.
99US-00234182.
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                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-605694/57
                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003021790-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-1998;
                                                                                                                                                                                                                                                    18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2003
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This interaction describes a movel, vaccine (VI) and/or an antibody, or comprising DNA (1) and/or an antibody, or completely imitates CDA, is new. (1) encodes a region of an antidotypic antibody (Ab2) or another peptide which: (a) specifically binds to the binding site of an antibody (Ab1) or an antigon of peptide which is an antigon of specifically binds to the binding site of an antibody (Ab1) or an antigon binding molecule; and (b) immunologically mimics the initial antigen. The binding molecule; and (b) immunologically mimics the initial antigen. The products is partially or completely conformation-dependent, and has an immunogenic structure defined by a specific spatial conformation of adds. (I) is used in the form of linear or dirular naked DNA and/or atth a viral vector and/or adjuvants. The products of the invention have cytostatic, virucidal, antibacterial and antiparasitic. The invention also describes (1) a corresponding vaccine (V2) against antigens which are not proteins or peptides, as defined above but which have epitopes which have an immunogenic structure; (2) preparing (V1) and (V2); (3) than antidiotypic antibody fragments against the MUC1-conformation epitope having one of 31 approximately 60 residue amino acids sequences, all fully defined in the specification; (4) MUC1-conformation epitope mimics having one of 16 9-17 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics thating one of 25 7-13 residue amino acid sequences, all fully defined in the specification; (6) TF carbohydrate epitope mimetics the specification; and (7) DNA sequences encoding the fragments and cancer, and infectious diseases, a cancer, and infectious diseases, cancer, and infectious diseases.
                                                                                                                                                                                                                                                                                                          MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer; antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen; antiparasitic; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccines against conformation-dependent or non-peptide antigens, based on 
DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel vaccine (V1) against conformation-
61 SRFSGSGSGTDFTLTISSLQPEDFATYYCQQHNEYPLTFGQGTKVEIKR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 5-9; 36pp; German.
                                                                                                                            AAB46020 standard; peptide; 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2000; 2000WO-DE001809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DE-01024405
99DE-01043016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          previously not been possible
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                     Human MUC-1 scFv clone N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karsten U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-049937/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200073430-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999;
09-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccines.
                                                                                                                                                                           AAB46020;
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91.4%; Score 512; DB 4; Length 240;

Query Match

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Indels

Local Similarity tes 107; Conservative

Best Loca Matches

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DIOMTOSPSSLSASVGDRVTITCRASKTISKYLAWYQQKPGKAPKLLI-YSGSTLQSGVP

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Best Local Similarity 91.7%; Pred. No. 2.8e-29;
Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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